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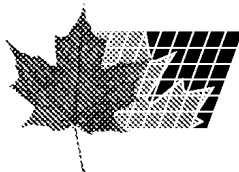
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(54) **ANTICORPS RECOMBINES ANTI-GPIIB/IIIA**
(54) **ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES**

(57)

The invention relates to novel nucleic acid sequences which code for human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane proteins. The invention also relates to new amino acid sequences of human antibodies and to the use thereof in the diagnosis and therapy of diseases.



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(54) **ANTICORPS RECOMBINES ANTI-GPIIB/IIIA**
(54) **ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES**

(57) L'invention concerne de nouvelles séquences d'acide nucléique qui codent pour des auto-anticorps et des anticorps anti-idiotypes humains contre la protéine membranaire d'agrégation plaquettaire, de nouvelles séquences aminoacides d'anticorps humains et leur utilisation pour le diagnostic et la thérapie de maladies.

(57) The invention relates to novel nucleic acid sequences which code for human auto-antibodies and anti-idiotypic antibodies against blood platelet membrane proteins. The invention also relates to new amino acid sequences of human antibodies and to the use thereof in the diagnosis and therapy of diseases.

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Abstract

The invention relates to novel nucleic acid sequences which encode human autoantibodies and antiidiotypic antibodies against blood platelet membrane proteins, to novel amino acid sequences of human antibodies, and to their use for the diagnosis and therapy of diseases.

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RECOMBINANT ANTI-GPIIB/IIIA ANTIBODIES

DESCRIPTION

5 The invention relates to novel nucleic acid sequences which encode human autoantibodies against blood platelet membrane proteins and which encode antiidiotypic antibodies, to novel amino acid sequences of human antibodies, and to their use for the diagnosis
10 and therapy of diseases.

Autoimmune thrombocytopenic purpura (AITP) is an immune disease which is defined by a low blood platelet count associated with normal or elevated megakaryocyto-
15 poiesis. The destruction of platelets in the reticuloendothelial system (spleen, liver and bone marrow) is increased due to the presence of anti-platelet autoantibodies. These autoantibodies, which can be detected in about 75% of AITP patients, are
20 predominantly directed against the platelet membrane glycoproteins (GP) IIb/IIIa and Ib/IX. Several different autoantibody specificities may be found in one and the same patient (cf., e.g., Berchtold and Wenger, Blood 81 (1993), 1246-1250; Kiefel et al., Br.
25 J. Haematol. 79 (1991), 256-262; McMillan et al., Blood 70 (1987), 1040 and Fujisawa et al., Blood 79 (1991); 1441). However, it is still difficult to characterize binding epitopes and to ascertain the pathogenic significance of the autoantibodies due to the limited
30 quantity of autoantibodies which can be obtained from AITP patients. It has only been possible to obtain a few human monoclonal antibodies from lymphocytes of AITP patients which react with GPIIb/IIIa AITP using the hybridoma technique (Kunicki et al., Hum. Antibodies Hybridomas
35 1 (1990) 83-95).

Natural autoantibodies against various selfantigens, for example against intracellular and cytoskeletal

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components of human platelets, have also been reported to occur in healthy individuals (Guilbert et al., J. Immunol. 128 (1982), 2779-2787; Hurez et al., Eur. J. Immunol. 23 (1993), 783-789 and Pfueller et al., Clin. Exp. Immunol. 79 (1990), 367-373). Some of these autoantibodies which have been observed in sera from healthy individuals can also be directed against platelet-membrane proteins (Souberbielle, Eur. J. Haematol. 56 (1996), 178-180). However, the role of these natural autoantibodies, and there relationship to disease-associated autoantibodies, is still unknown.

Corticosteroids can be used for treating AITP. About half of the patients react within 4 weeks to an administration of prednisone; however long-term remissions are only rarely seen. The administration of high doses of intravenous immunoglobulin (IVIgG) is recommended as an emergency treatment for patients who are exhibiting severe bleeding or extremely low platelet counts. This treatment is followed in most patients by a rapid, but usually only transient, increase in the platelet count. The mechanisms by which corticosteroids and IVIgG act in the treatment of AITP are still unknown. Investigations carried out by Berchtold et al., (Blood 74 (1989), 2414-2417 and Berchtold and Wenger, Blood 81 (1993), 1246-1250) have disclosed that antiidiotypic antibodies which are present in IVIgG can inhibit the binding of autoantibodies to platelet glycoproteins.

The problem underlying the present application is that of identifying novel DNA sequences which are responsible for autoantibodies binding to GPIIb/IIIa. This approach can be used for making available novel pharmaceutical preparations which can be employed for improving the diagnosis and therapy of AITP.

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It was surprisingly possible to identify binding sequences from autoantibodies after using peripheral circulating B cells from a healthy human donor to prepare a combinatorial phagemid display library of human antibody heavy and light chains. Following the presentation of human heavy and light antibody Fab fragments on the surface of the filamentous phage M13, it was possible to identify phage clones which exhibit specific binding to GPIIb/IIIa.

For this, the phagemid library was brought consecutively into contact with thrombasthenic platelets lacking GPIIb/IIIa (negative selection) and normal platelets (positive selection). After several rounds of selection and amplification by infecting E.coli, 23 clones were obtained which were able to bind to the GPIIb/IIIa complex. Inhibition studies using pools of monoclonal antibodies directed against the GPIIb/IIIa yielded two groups of clones: both groups were inhibited by monoclonal antibodies which were specific for the GPIIb/IIIa complex and one group was also inhibited by a GPIIb-specific monoclonal antibody. These findings were confirmed by carrying out a DNA analysis of the clones which indicated the presence of 2 different anti-GPIIb/IIIa phage clones. These results demonstrate that 2 GPIIb/IIIa-specific phage clones, i.e. autoantibodies, can be cloned from the genome of a healthy individual and that these clones are able to recognize conformational epitopes belonging to the GPIIb/IIIa complex. Inhibition studies furthermore established that both phage clones inhibit the binding of platelet-associated autoantibodies from AITP patients to purified GPIIb/IIIa and therefore presumably recognize GPIIb/IIIa epitopes which are AITP-associated. Since the phage clones contain the antigen-binding sequences of natural autoantibodies which are derived from the genome of a healthy individual, this finding can lead to new insights into

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the origin of platelet-associated autoantibodies in AITP.

In addition to this, it is possible to use the novel
5 phage clones to produce recombinant antiidiotypic
antibodies against anti-GPIIb/IIIa autoantibodies, with
the anti-GPIIb/IIIa phage clones being used as antigen.
The recombinant antiidiotypic antibodies which can be
obtained in this way constitute an attractive clinical
10 alternative to using IVIgG.

The nucleotide sequences of the identified phage
clones, and the amino acid sequences which are deduced
from these nucleotide sequences, are depicted in the
15 sequencing listings SEQ ID No. 1 to 8 (autoantibodies)
and SEQ ID No. 9 to 18 (antiidiotypic antibodies).

I. Autoantibodies

20 A first aspect of the present invention relates to
nucleic acids which encode auto-antibodies. Part of the
subject-matter of the invention is therefore a nucleic
acid which encodes the heavy chain of a human antibody,
or a functional derivative or a fragment thereof, and
25 encompasses a CDR3 region, selected from:

- (a) a nucleotide sequence which encodes the amino
acid sequence:
V L P F D P I S M D V, (I)
- (b) a nucleotide sequence which encodes the amino
30 acid sequence:
A L G S W G G W D H Y M D V, (II)
- (c) a nucleotide sequence which encodes an amino
acid sequence having an homology of at least 80%, and
preferably at least 90%, with an amino acid
35 sequence from (a) or (b), and
- (d) a nucleotide sequence which encodes an amino
acid sequence having an equivalent ability to
bind to GPIIb/IIIa.

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The novel nucleic acid furthermore preferably comprises a CDR1 region selected from:

- 5 (a) a nucleotide sequence which encodes the amino acid sequence:
G Y S W R, (III)
- (b) a nucleotide sequence which encodes the amino acid sequence:
S Y A M H, (IV)
- 10 and
- (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with an amino acid sequence from (a) or (b).

15

The novel nucleic acid preferably furthermore comprises a CDR2 region selected from:

- (a) a nucleotide sequence which encodes the amino acid sequence:
20 D I S Y S G S T K Y K P S L R S, (V)
- (b) a nucleotide sequence which encodes the amino acid sequence:
V I S Y D G S N K Y Y A D S V K G, (VI)
- and
- 25 (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably of at least 90%, with an amino acid sequence from (a) or (b).

30 A second aspect of the present invention is a nucleic acid which encodes the light chain of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:

- 35 (a) a nucleotide sequence which encodes the amino acid sequence:
A T W D D G L N G P V, (VII)
- (b) a nucleotide sequence which encodes the amino acid sequence:

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A A W D D S L N G W V, (VIII)

- (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably of at least 90%, with an amino acid sequence from (a) or (b), and
- (d) a nucleotide sequence which encodes an amino acid sequence having an equivalent ability to bind to GPIIb/IIIa.

10 The novel nucleic acid preferably furthermore comprises a CDR1 region selected from:

- (a) a nucleotide sequence which encodes the amino acid sequence:
S G S S S N I R S N P V S, (IX)
- 15 (b) a nucleotide sequence which encodes the amino acid sequence:
S G S S S N I G S N T V N, (X)
and
- (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with an amino acid sequence from (a) or (b).

25 In addition, the novel nucleic acid preferably further comprises a CDR2 region selected from:

- (a) a nucleotide sequence which encodes the amino acid sequence:
G S H Q R P S, (XI)
- (b) a nucleotide sequence which encodes the amino acid sequence:
30 S N N Q R P S, (XII)
and
- (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with an amino acid sequence from (a) or (b).

II. Antiidiotypic antibodies

A second aspect of the present invention relates to nucleic acids which encode antiidiotypic antibodies.

5 Part of the subject-matter of the invention is therefore a nucleic acid which encodes the heavy chain of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:

- 10 (a) a nucleotide sequence which encodes the amino acid sequence:
V R D L G Y R V L S T F T F D I, (XIII)
- (b) a nucleotide sequence which encodes the amino acid sequence:
15 D G R S G S Y A R F D G M D V, (XIV)
- (c) a nucleotide sequence which encodes the amino acid sequence:
M G S S V V A T Y N A F D I, (XV)
- (d) a nucleotide sequence which encodes the amino acid sequence:
20 D A D G D G F S P Y Y F P Y, (XVI)
- (e) a nucleotide sequence which encodes the amino acid sequence:
L R N D G W N D G F D I, (XVII)
- 25 (f) a nucleotide sequence which encodes the amino acid sequence:
D S E T A I A A A G R F D I, (XVIII)
- (g) a nucleotide sequence which encodes the amino acid sequence:
30 E D G T T V P S Q P L E F, (XIX)
- (h) a nucleotide sequence which encodes the amino acid sequence:
G S G S Y L G Y Y F D Y, (XX)
- (i) a nucleotide sequence which encodes the amino acid sequence:
35 G L R S Y N Y G R N L D Y, (XXI)
- (j) a nucleotide sequence which encodes an amino acid sequence having an homology of at least

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80%, and preferably of at least 90%, with an amino acid sequence from (a), (b), (c) or (d), and

- 5 (k) a nucleotide sequence which encodes an amino acid sequence having an equivalent ability to bind to autoantibodies against GPIIb/IIIa.

The novel nucleic acid furthermore preferably comprises a CDR1 region selected from: a nucleotide
10 sequence which encodes the amino acid sequences N F A M S, S Y T M H, D Y A L H or S H Y W S shown in Tab. 7a, a nucleotide sequence which encodes the amino acid sequence T Y Y W S, a nucleotide sequence which encodes the amino acid sequences D Y G M H, S H T I S,
15 K Y A I H or E L S M H shown in Tab. 7b, and a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with one of the previously mentioned amino acid sequences.

20 Preferably, the novel nucleic acid furthermore comprises a CDR2 region selected from a nucleotide sequence which encodes the amino acid sequences G I S G G G L L T H Y A (D/N) S V K G, L I S Y D G S N K Y Y A
25 D S V K G, G I S W D S T S I G Y A D S V K G or F I Y D G A R T R F N P S L R S shown in Tab. 7a, a nucleotide sequence which encodes the amino acid sequence Y I Y S G N T N Y N P S L K S, a nucleotide sequence which encodes the amino acid sequences A I S Y D G S N K Y Y A D S V
30 K G, G I T P I F G T V N Y A Q K F Q G, A I S S N G G N T Y Y A D S V K G or G F D P E D G E T I Y A Q K F Q G shown in Tab. 7b, and a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably of at least 90%, with one of
35 the previously mentioned amino acid sequences.

Another part of the subject-matter of the present invention is a nucleic acid which encodes the light

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chain of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:

- 5 (a) a nucleotide sequence which encodes the amino acid sequence:
C S Y V H S S T N, (XXII)
- (b) a nucleotide sequence which encodes the amino acid sequence:
Q V W D N T N D Q, (XXIII)
- 10 (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with an amino acid sequence from (a), and
- 15 (d) a nucleotide sequence which encodes an amino acid sequence having an equivalent ability to bind to autoantibodies against GPIIb/IIIa.

Preferably, the novel nucleic acid furthermore comprises a CDR1 region selected from a nucleotide
20 sequence which encodes the amino acid sequence T G T S S A I G N Y N F V P shown in Tab. 7a, a nucleotide sequence which encodes the amino acid sequence G G Y K I G S K S V H shown in Tab. 7b, and a nucleotide
25 sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably of at least 90%, with the previously mentioned amino acid sequence.

In addition, the novel nucleic acid preferably furthermore comprises a CDR2 region selected from a
30 nucleotide sequence which encodes the amino acid sequence E G S K R P S shown in Tab. 7a, a nucleotide sequence which encodes the amino acid sequence E D S Y R P S shown in Tab. 7b, and a nucleotide sequence which
35 encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with the previously mentioned amino acid sequence.

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Within the meaning of the present invention, the phrase "functional derivative of a chain of a human antibody" is to be understood as meaning a polypeptide which encompasses at least a CDR3 region of the heavy and/or light chain, as defined above, and which is able, where appropriate together with the relevant complementary chain of the human antibody (or a derivative of such a chain), to form an antibody derivative which possesses a recognition specificity for an antigen which is equivalent to that possessed by the non-derivatized antibody. Preferably, such an antibody derivative has a binding constant for the relevant antigen of at least 10^{-5} l/mol, preferably of at least 10^{-3} l/mol.

Functional derivatives of chains of a human antibody can be prepared, for example, by using recombinant DNA techniques to delete, substitute and/or insert segments of the gene encoding the relevant polypeptide.

Single-chain antibodies, which can, for example, be composed of the variable domains of the H and L chains or one or two H chain domains and, where appropriate a constant domain, are particularly preferred functional derivatives of antibody chains or antibodies. The preparation of such constructs is described in Hoogenboom et al., Immunol. Rev. 130 (1992), 41-68; Barbas III, Methods: Companion Methods Enzymol. 2 (1991), 119 and Plückthun, Immunochemistry (1994), Marcel Dekker Inc., Chapter 9, 210-235.

Within the meaning of the present invention, the phrase "equivalent ability to bind" is to be understood as being a binding affinity and/or specificity, i.e. epitope recognition, which is the same as that in the specifically disclosed sequences.

Another part of the subject-matter of the present invention is a vector which contains at least one copy

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of a novel nucleic acid. This vector can be a prokaryotic vector or a eukaryotic vector. Plasmids, cosmids and bacteriophages are examples of prokaryotic vectors. Such vectors are, for example, described in
5 detail in Chapters 1 to 4 in Sambrook et al., Molecular Cloning. A Laboratory Manual, 2nd edition (1989), Cold Spring Harbor Laboratory Press. A prokaryotic vector is preferably a plasmid or a phage.

10 On the other hand, the vector can also be a eukaryotic vector, e.g. a yeast vector, an insect vector (baculovirus) or a mammalian vector (plasmid vector or viral vector). Examples of eukaryotic vectors are described in Sambrook et al., loc. cit., Chapter 16,
15 and Winnacker, Gene und Klone, Eine Einführung für die Gentechnologie [Genes and clones, an introduction to genetic engineering] (1985), VCH Verlagsgesellschaft, in particular Chapters 5, 8 and 10.

20 Yet another part of the subject-matter of the present invention is a cell which expresses a novel nucleic acid, or a cell which is transformed with a novel nucleic acid or with a novel vector. The cell can be a prokaryotic cell (e.g. a Gram-negative bacterial cell,
25 in particular E.coli) or a eukaryotic cell (e.g. a yeast, plant or mammalian cell). Examples of suitable cells and methods for introducing the novel nucleic acid into such cells can be found in the above literature references.

30 Another part of the subject-matter of the present invention is a polypeptide which is encoded by a novel nucleic acid, in particular a recombinant polypeptide. Particularly preferably, the polypeptide contains the
35 variable domain of the H chain and/or L chain of a human antibody.

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Particular preference is given to a polypeptide which exhibits antibody properties and whose subunit components are a heavy chain, or a functional derivative thereof, and a light chain, or a functional derivative thereof. The polypeptide can be composed of two separate chains or be present as a single-chain polypeptide.

Yet another part of the subject-matter of the present invention is an antibody against a novel polypeptide, which antibody is directed against a region of the polypeptide which is responsible for recognizing the antigen. This antibody can be a polyclonal antiserum, a monoclonal antibody or a fragment of a polyclonal or monoclonal antibody (e.g. a Fab, $F(ab)_2$, Fab' or $F(ab')_2$ fragment). The antibody is preferably directed against the CDR3 region of the heavy and/or light antibody chain of the novel polypeptide, or a region thereof. Known methods can be used to obtain such antibodies by immunizing an experimental animal with a peptide or polypeptide which contains a novel CDR3 region and isolating the resulting polyclonal antibody from the experimental animal. In addition, monoclonal antibodies can be obtained by fusing an antibody-producing B cell from the experimental animal with a leukaemia cell in accordance with the method of Köhler and Milstein or a further development of this method. In addition, recombinant antibodies which are directed against the CDR3 region of the novel polypeptide can also be obtained by screening a suitable phagemid library, e.g. a phagemid library from a healthy human donor, with a novel polypeptide being used as the antigen.

The invention also relates to a pharmaceutical composition which comprises a nucleic acid, a vector, a polypeptide, an antibody or a cell as previously mentioned, as active component, where appropriate together with other active components and also

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pharmaceutically customary adjuvants, additives or excipients.

5 The pharmaceutical composition can be used for preparing a diagnostic or therapeutic agent. Examples of diagnostic uses are the diagnosis of AITP or of a predisposition for AITP. Another preferred diagnostic use is that of monitoring the course of the AITP disease.

10

The use of the pharmaceutical composition as a diagnostic agent can comprise, for example, detecting a B cell subpopulation which is expressing a novel polypeptide as the antibody. This antibody can be
15 detected, for example, at the nucleic acid level, e.g. by means of a nucleic-acid-hybridization assay, together with prior amplification where appropriate. On the other hand, the antibody can also be detected as to the protein level by means of an immunoassay using
20 antigens or antibodies which react specifically with the polypeptide.

Furthermore, the novel pharmaceutical composition can also be applied in the therapeutic field, in particular
25 for the prevention or therapy of AITP. This therapeutic use can, for example, be based on stimulating the production of anti-autoantibodies. For this, the novel autoantibody polypeptide can, for example, be administered to a patient, thereby eliciting and/or
30 stimulating the formation of antiidiotypic antibodies. In this connection, this administration can be effected in accordance with customary immunization protocols (Fox et al., J. Pharmacol. Exp. Ther. 279 (1996), 1000-1008; Whittum-Hudson et al., Nat. Med. 2 (1996),
35 1116-1121; Jardieu, Curr. Opin. Immunol. 7 (1995), 779-782). On the other hand, the expression of antibody genes can be inhibited specifically by administering suitable antisense nucleic acids. The novel

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antiidiotypic antibody polypeptide can be administered to a patient in order to achieve direct inhibition of the autoantibody activity.

- 5 Investigations carried out on the novel autoantibody polypeptides have shown that these polypeptides are surprisingly able to inhibit the binding of fibrinogen to blood platelets. The novel autoantibody polypeptides and antiidiotypic antibody polypeptides can therefore
10 be employed, where appropriate in combination, as agents for modulating blood coagulation, in particular for preventing a thrombosis, for example following cardiac infarctions or strokes, or in association with venous thromboses together with lung embolisms or
15 ischaemias, etc.

Murine monoclonal antibodies, e.g. the monoclonal antibody 7E3 (cf., e.g., US patent 5,440,020) or fragments thereof (e.g. the commercially available Fab
20 fragment ReoPro®), or short synthetic peptides, have hitherto been used as fibrinogen antagonists for therapeutic purposes. However, murine monoclonal antibodies and antibody fragments suffer from the disadvantage that, as a result of their immunogenicity,
25 they give rise to undesirable side reactions when used for treating human patients, while short peptides are generally degraded very rapidly. As compared with these known agents, the novel polypeptides have the advantage that they consist of amino acid sequences of human
30 origin and therefore exhibit fewer undesirable side effects than do corresponding murine antibodies or antibody fragments, and that, because of their size, they are not subjected to such rapid degradation as are peptides.

35

The invention therefore relates to the use of a novel nucleic acid, in particular a nucleic acid which encodes an autoantibody polypeptide, of a vector which

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contains this nucleic acid, of a cell which is transformed with the nucleic acid or the vector, of a polypeptide which is encoded by the nucleic acid, or of a pharmaceutical composition which comprises one or more of the said substances, for preparing an agent for affecting and in particular inhibiting the binding of fibrinogen to blood platelets. Preference is given to using the agent for modulating blood coagulation, in particular for dissolving thrombi and/or for preventing the formation of thrombi. The administration of the novel pharmaceutical composition can be effected in accordance with protocols which have already been established for murine antibodies or antibody fragments.

Yet another part of the subject-matter of the invention is a process for isolating phagemid clones which express nucleic acids which encode autoantibodies against GPIIb/IIIa or encode antiidiotypic antibodies which are directed against these autoantibodies, characterized in that a phagemid library is prepared from lymphocytes from a human donor and the desired phagemid clones are isolated by affinity selection, comprising negative and positive selection steps. Preferably, the process also involves isolating antibody-encoding nucleic acids from the clones and/or using the antibody-encoding nucleic acids for expressing recombinant antibody chains or derivatives or fragments thereof.

The invention is also explained by the following examples, figures and sequence listings, in which

SEQ ID No. 1 shows the nucleotide sequence of the H chain of a novel antibody (phagemid clone PDG7), with framework region (FR)1 extending from bp 1 to 90, complement-determining region (CDR)1 from bp 91 to

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105, FR2 from bp 106 to 147, CDR2 from bp 148 to 195, FR3 from bp 196 to 291, CDR3 from bp 292 to 324 and FR4 from bp 325 to 357,

5

SEQ ID No.2 shows the amino acid sequence corresponding to the nucleotide sequence depicted in SEQ ID No.1, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 65, FR3 from AA 66 to 97, CDR3 from AA 98 to 108 and FR4 from AA 109 to 119,

10

15 SEQ ID No.3 shows the nucleotide sequence of the L chain of a novel polypeptide (phagemid clone PDG7), with FR1 extending from bp 1 to 60, CDR1 from bp 61 to 99, FR2 from bp 100 to 144, CDR2 from bp 145 to 165, FR3 from bp 166 to 261, CDR3 from bp 262 to 294 and FR4 from bp 295 to 333,

20

SEQ ID No.4 shows the amino acid sequence corresponding to the nucleotide sequence given in SEQ ID No. 3, with FR1 extending from AA 1 to 20, CDR1 from AA 21 to 33, FR2 from AA 34 to 48, CDR2 from AA 49 to 55, FR3 from AA 56 to 87, CDR3 from AA 88 to 98 and FR4 from AA 99 to 11 [sic],

25

30

SEQ ID No.5 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone PDG13), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 109, FR2 from bp 106 to 147, CDR2 from bp 148 to 198, FR3 from bp 199 to 294, CDR3 from

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bp 295 to 336 and FR4 from bp 337 to 369,

5 SEQ ID No.6 shows the amino sequence corresponding
to the nucleotide sequence depicted in
SEQ ID No.5, with FR1 extending from AA
1 to 30, CDR1 from AA 31 to 35, FR2 from
AA 36 to 49, CD2 from AA 50 to 66, FR3
10 from AA 67 to 98, CDR3 from AA 99 to 112
and FR4 from AA 113 to 123,

15 SEQ ID No.7 shows the nucleotide sequence of the L
chain of a novel polypeptide (phagemid
clone PGD13), with FR1 extending from
bp 1 to 60, CDR1 from bp 61 to 99, FR2
from bp 100 to 144, CDR2 from bp 145 to
165, FR3 from bp 166 to 261, CDR3 from
bp 262 to 294 and FR4 from bp 295 to
20 333,

25 SEQ ID No.8 shows the amino acid sequence of the
nucleotide sequence depicted in SEQ ID
No. 7, with FR1 extending from AA 1 to
20, CDR1 from AA 21 to 33, FR2 from AA
34 to 48, CDR2 from AA 49 to 55, FR3
from AA 56 to 87, CDR3 from AA 88 to 98
and FR4 from AA 99 to 111,

30 SEQ ID No.9 shows the nucleotide sequence of the H
chain of a novel polypeptide (phagemid
clone AI-X16), with FR1 extending from
bp 1 to 90, CDR1 from bp 91 to 105, FR2
from bp 106 to 147, CDR2 from bp 148 to
198, FR3 from bp 199 to 288, CDR3 from
35 bp 289 to 336 and FR4 from bp 337 to
369,

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- 5 SEQ ID No.10 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 9, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 66, FR3 from AA 67 to 96, CDR3 from AA 97 to 112 and FR4 from AA 113 to 123,
- 10 SEQ ID No. 11 shows the nucleotide sequence of the L chain of a novel polypeptide (phagemid clone AI-X16), with FR1 extending from bp 1 to 60, CDR1 from bp 61 to 102, FR2 from bp 103 to 147, CDR2 from bp 148 to 168, FR3 from bp 169 to 264, CDR3 from [lacuna] 265 to 291 and FR4 from bp 292 to 375,
- 15 SEQ ID No. 12 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 11, with FR1 extending from AA 1 to 20, CDR1 from AA 21 to 34, FR2 from AA 35 to 49, CDR2 from AA 50 to 56, FR3 from AA 57 to 88, CDR3 from AA 89 to 97 and FR4 from AA 89 to 125,
- 20 SEQ ID No. 13 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-X20), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 195, FR3 from bp 196 to 291, CDR3 from bp 292 to 333 and FR4 from bp 334 to 366,
- 25 SEQ ID No. 14 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 13, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA
- 30 SEQ ID No. 14 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 13, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA
- 35 SEQ ID No. 14 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 13, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA

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36 to 49, CDR2 from AA 50 to 65, FR3 from AA 66 to 97, CDR3 from AA 98 to 111 and FR4 from AA 112 to 122,

5 SEQ ID No. 15 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-X39), with FR extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from pb [sic] 148 to 198, FR3 from bp 199 to 294, CDR3 from bp 295 to 339 and FR4 from 340 to 372,

15 SEQ ID No. 16 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 15, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 66, FR3 from AA 67 to 98, CDR3 from AA 99 to 113 and FR 4 from AA 114 to 124,

25 SEQ ID No. 17 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-X40), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 198, FR3 from bp 199 to 297, CDR3 from bp 298 to 339 and FR4 from bp 340 to 372,

30 SEQ ID No. 18 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 17, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 66, FR3 from AA 67 to 99, CDR3 from AA 100 to 113 and FR4 from AA 114 to 124,

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- 5 SEQ ID No. 19 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-X2), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 195, FR3 from bp 196 to 291, CDR3 from bp 292 to 327 and FR4 from bp 328 to 360,
- 10 SEQ ID No. 20 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 19, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 65, FR3 from AA 66 to 97, CDR3 from AA 98 to 109 and FR4 from AA 110 to 120,
- 15
- 20 SEQ ID No. 21 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-B14), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 198, FR3 from bp 199 to 294, CDR3 from bp 295 to 336 and FR4 from bp 337 to 369;
- 25

30 The following variations in the sequence were also found: a C can be present at position 7, while a G can be present at position 9, a G at position 13, a G at position 15, an A at position 91, a G at position 92, a C at position 98, a T at position 149, an A at position 205, an A at position 228, an A at position 251, a T at position 253 and/or an A at position 284. The consequence of this is that, in the amino acid sequence (cf. SEQ ID No. 22), a Q can be present at

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5 position 3, while a V can be present at position 5, an S at position 31, an A at position 33, a V at position 50, a T at position 69, a K at position 76, an N at position 84, an S at position 85 and/or a Y at position 95.

10 SEQ ID No. 22 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 21, with FR1 extending from AA 1 to 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 66, FR3 from AA 67 to 98, CDR3 from AA 99 to 112 and FR4 from AA 113 to 123,

15 SEQ ID No. 23 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-B18), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 198, FR3 from bp 199 to 294, CDR3 from bp 295 to 333 and FR4 from bp 334 to 366;

25 The following variations in the nucleotide sequence were also found: thus, a C can be present at position 7, while a G can be present at position 13, a C at position 16, an A at position 56, 30 a T at position 94, a G at position 97, a T at position 155, a C at position 173, a T at position 223, a T or a C at position 252, a G at position 261, a G at position 267, an A at position 271, a 35 C at position 275 and/or a G at position 277. The consequence of this is that, in the corresponding amino acid sequence (cf. SEQ ID No. 24), a Q can be present

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5 at position 3, while a V can be present
at position 5, a Q at position 6, a K at
position 19, a Y at position 32, an A at
position 33, an I at position 52, an A
at position 58, an S at position 75, an
S at position 84, an R at position 87,
an E at position 89, a T at position 91,
an A at position 92 and/or a V at
position 93.

10

SEQ ID No. 24 shows the amino acid sequence of the
nucleotide sequence depicted in SEQ ID
No. 23, with FR1 extending from AA 1 to
30, CDR1 from AA 31 to 35, FR2 from
15 AA 36 to 49, CDR2 from AA 50 to 66, FR3
from AA 67 to 98, CDR2 from AA 99 to 111
and FR4 from AA 112 to 122,

20

SEQ ID No. 25 shows the nucleotide sequence of the H
chain of a novel polypeptide (phagemid
clone AI-B24), with FR1 extending from
bp 1 to 90, CDR1 from bp 91 to 105, FR2
from bp 106 to 147, CDR2 from bp 148 to
198, FR3 from bp 199 to 294, CDR3 from
25 bp 295 to 330 and FR4 from bp 331 to
363;

30

The following variations in the
nucleotide sequence were also found: a C
can be present at position 7, while a G
can be present at position 9, a G at
position 13, a G at position 15, a G at
position 31, an A at position 46, a G at
position 67, a G at position 89, a G at
35 position 92, a C at position 93, a G at
position 98, a G at position 102, a G at
position 140, a G at position 141, a G
at position 145, a T at position 149, a

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5 T at position 157, an A at position 158,
a G at position 160, an A at position
166, an A at position 173, a T at
position 235, an A at position 251, a C
at position 290 and/or an A at position
293. The consequence of this is that, in
the corresponding amino acid sequence
(cf. SEQ ID No. 26), a Q can be present
at position 3, while a V can be present
10 at position 5, a V at position 11, an R
at position 16, an A at position 23, an
S at position 30, an S at position 31, a
G at position 33, an M at position 34, a
W at position 47, an A at position 49, a
15 V at position 50, a Y at position 53, a
D at position 54, an S at position 56, a
K at position 58, an L at position 79,
an N at position 84, an A at position 97
and/or a K at position 98.

20 SEQ ID No. 26 shows the amino acid sequence of the
nucleotide sequence depicted in SEQ ID
No. 25, with FR1 extending from AA 1 to
30, CDR1 from AA 31 to 35, FR2 from
25 AA 36 to 49, CDR2 from AA 50 to 66, FR3
from AA 67 to 98, CDR3 from AA 99 to 110
and FR4 from AA 111 to 121,

30 SEQ ID No. 27 shows the nucleotide sequence of the L
chain of a novel polypeptide (phagemid
clone AI-B24), with FR1 extending from
bp 1 to 60, CDR1 from bp 61 to 96, FR2
from bp 97 to 138, CDR2 from bp 139 to
159, FR3 from bp 160 to 255, CDR3 from
35 bp 256 to 282 and FR4 from bp 283 to
366;

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The following variations in the nucleotide sequence were also found: a C or a T can be present at position 4, while a G can be present at position 37, an A at position 40, a G at position 50, an A at position 67, a T at position 72, an A at position 133, a T at position 136, a T or a C at position 138, a G at position 148, a T at position 160, a T at position 161, a T or a C at position 162, a C at position 200, a T at position 217, a G at position 218, an A or a C at position 220, a G at position 269, a T at position 271, a G at position 272, a G at position 275 and/or a T or a C at position 282. The consequence of this is that, in the corresponding amino acid sequence (cf. SEQ ID No. 28), an L can be present at position 2, while a G can be present at position 13, a K at position 14, an R at position 17, an N at position 23, an N at position 24, an I at position 45, a Y at position 47, a D at position 50, an F at position 54, a T at position 67, an S at position 73, an R at position 74, an S at position 90, an S at position 91, an S at position 92 and/or an H at position 94.

30

SEQ ID No. 28 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 27, with FR1 extending from AA 1 to 20, CDR1 from AA 21 to 32, FR2 from AA 33 to 46, CDR2 from AA 47 to 53, FR3 from AA 54 to 85, CDR3 from AA 86 to 94 and FR4 from AA 95 to 122,

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5 SEQ ID No. 29 shows the nucleotide sequence of the H chain of a novel polypeptide (phagemid clone AI-B38), with FR1 extending from bp 1 to 90, CDR1 from bp 91 to 105, FR2 from bp 106 to 147, CDR2 from bp 148 to 198, FR3 from bp 199 to 294, CDR3 from bp 295 to 333 and FR4 from bp 334 to 366;

10 The following variations in the nucleotide sequence were also found: a C can be present at position 7, while a G can be present at position 9, a G at position 13, an A at position 15 and/or
15 a C at position 16. The consequence of this is that, in the corresponding amino acid sequence, a Q can be present at position 3, while a V can be present at position 5 and/or a Q can be present at
20 position 6, and

SEQ ID No. 30 shows the amino acid sequence of the nucleotide sequence depicted in SEQ ID No. 29, with FR1 extending from AA 1 to
25 30, CDR1 from AA 31 to 35, FR2 from AA 36 to 49, CDR2 from AA 50 to 66, FR3 from AA 67 to 98, CDR3 from AA 99 to 111 and FR4 from AA 112 to 122.

30 Figure 1 shows the inhibition of the binding of autoantibody phabs (PDG-X) to GPIIb/IIIa which is brought about by adding the antiidiotypic antibody phab AI-X17.

35 Figure 2 shows the inhibition of the binding of autoantibody phabs (PDG-B) to blood platelets which is brought about by antiidiotypic antibody phabs AI-B,

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Figure 3 shows the binding of autoantibody phabs to untreated and EDTA-treated blood platelets,

5 Figure 4 shows the inhibition of the binding of fibrinogen to GPIIb/IIIa which is brought about by autoantibody phabs,

10 Figures 5-7 show the inhibition of the binding of autoantibody phabs to GPIIb/IIIa which is brought about by the antibody 7E3 and the antibody fragment ReoPro®.

Examples

15

1. Identification of autoantibody sequences

1.1. Isolation of autoantibodies

20 Autoantibodies were obtained from 12 AITP patients (8 suffering from primary AITP, 3 suffering from AITP associated with SLE, 1 suffering from AITP associated with Sjögren's syndrome) by incubating patient plasma with purified GPIIb/IIIa at 4°C overnight and
25 subsequently eluting, at room temperature for 15 min, in 0.2 mol/l glycine and 0.15 mol/l NaCl, pH 2.5. After centrifuging at 100,000 g for 30 min, the supernatant was neutralized with 1 mol/l Tris-HCl and dialysed overnight against Tris-buffered salt solution (TBS).

30

At the time of plasma withdrawal, all the patients were thrombocytopenic (platelet count $< 150 \times 10^9/l$) and had normal or enlarged megakaryocytes in the bone marrow and were free of other detectable forms of
35 immunothrombocytopenia.

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1.2. Isolation of purified antigens

The antigens used were purified GPIIb/IIIa, a cytoplasmic fragment of GPIIIa (amino acids 721-744) and an extracellular fragment of GPIIIa (amino acids 468-690) (Beardsley, Blut 59 (1989), 47-51 and Phillips et al., Methods Enzymol. 215 (1992), 244-263).

1.3. Isolation of platelets for panning and immunoblotting

Platelet-enriched plasma was prepared by differential centrifugation from EDTA-anticoagulated blood samples taken from healthy human donors. The platelets were isolated by centrifuging at 2000 g for 15 min, then washed six times in citric acid buffer (pH 6.2) containing 50 mmol/l sodium citrate, 100 mmol/l NaCl and 125 mmol/l glucose, and finally resuspended in the same buffer.

The same enrichment protocol was used to obtain thrombasthenic platelets from a 14-year-old boy suffering from Glanzmann's type I thrombasthenia.

1.4. Monoclonal antibodies

Use was made of murine monoclonal antibodies which recognize the complexed form of GPIIb/IIIa and of antibodies which recognize GPIIb or GPIIIa selectively. These antibodies were isolated by means of customary immunization protocols using the corresponding antigens and are not AITP-associated. The isolation of such antibodies is described in Kouns et al. (J. Biol. Chem. 267 (1992), 18844-18851), Steiner et al. (Biochim. Biophys. Acta 1119 (1992), 12-21) and Häring et al. (Proc. Natl. Acad. Sci. USA 82 (1985), 4837-4841).

1.5. Phagemid library

A combinatorial Fab library was prepared in accordance with the method described by Vogel et al. (Eur. J. Immunol. 24 (1994), 1200-1207) using peripheral blood lymphocytes obtained from a healthy, preimmunized human donor. All the enzymes and oligonucleotides were obtained from Boehringer Mannheim GmbH (Mannheim, Germany) apart from the Taq polymerase (Perkin Elmer, NJ, USA). The primers for amplifying the H and L chains of the Fab molecules by PCR, the VCSM13 helper phage, and the Escherichia coli strain XL-Blue were obtained from Stratagene (La Jolla, CA, USA). The phagemid pComb3 was obtained from Scripps Research Institute (La Jolla, CA, USA). The cloning, the transformation into XL-Blue cells and the preparation of phabs were carried out as described by Barbas III and Lerner, Methods: Companion Methods Enzymol. 2 (1991), 119). The phabs were precipitated with 4% (w/v) polyethylene glycol 8000 and 3% (w/v) NaCl and resuspended in PBS, pH 7.4. The resulting expression library contains 1×10^7 specificities.

1.6. Isolation of GPIIb/IIIa-specific phabs

GPIIb/IIIa-specific phabs were prepared by means of a total of 5 rounds of an affinity selection ("panning"). Following preabsorption (negative selection) with 5×10^7 thrombasthenic platelets, the phabs were incubated for 45 min with 10^8 normal platelets (positive selection). Bound phabs were then eluted with 0.05 mol/l sodium citrate, pH 2.5, and neutralized with 1 mol/l Tris buffer. After each round of panning, the enrichment of GPIIb/IIIa-specific phabs was monitored by titrating the phage-colony-forming units. After five rounds of selection, the eluted phabs were found to have been enriched by a factor of more than 100.

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The pool of phabs obtained after the fourth round of selection was analysed more closely for its GPIIb/IIIa specificity. For this, 40 phab clones were selected at random and their binding specificity was ascertained in an immunodot assay. One μ l of normal and thrombasthenic platelets (10^9 ml) [sic], and also purified GPIIb/IIIa (500 μ g/ml), were added as drops onto nitrocellulose strips (Millipore Corporation, Bedford, MA, USA). The strips were blocked in TBS containing 0.15% casein (TBS-casein) and then incubated overnight together with the phabs, which had been diluted in TBS-casein. After three washes with TBS-0.1% Tween 20 (TBS-Tween), the bound phabs were detected with 4-chloro-1- α -naphthol (Merck, Darmstadt, Germany) following incubation with horseradish peroxidase-conjugated polyclonal rabbit anti-phage antibody (Vogel et al., loc. cit.) which had been diluted 1:1000 in TBS-casein.

The binding of phabs to platelets and purified GPIIb/IIIa was also tested after denaturing the proteins by heating (70°C) or by acid treatment (pH 2 with 0.5 N HCl) before dropping.

Of the 40 randomly selected clones, 23 (57.5%) reacted with GPIIb/IIIa, whereas 17 did not exhibit any binding. No binding of anti-GPIIb/IIIa [sic] to phabs was observed after denaturing the antigen by heat or pH 2 prior to the incubation, thereby demonstrating that intact GPIIb/IIIa is required for the phab binding. Determining the presence of Fab in negative phabs revealed that 15 of the clones (88%) did not contain any Fab molecules. The two Fab-positive clones which did not bind to GPIIb/IIIa could have a low binding affinity for GPIIb/IIIa.

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1.7. Fab analysis

In order to test the positive phabs for kappa (κ), lambda (λ) and Fd chains, the anti-GPIIb/IIIa phabs were added as drops to nitrocellulose. The filters were incubated for 4 hours with peroxidase-labelled mouse anti-human λ , κ (The Binding Site Limited, Birmingham, England) and Fd antibodies (from the HP6045 myeloma cell line, ATCC1757, Rockville, MD, USA), which antibodies had been diluted 1:1000 in TBS-casein, and then developed by chemiluminescence (ECL, Amersham, Switzerland, Zurich, Switzerland). Testing 15 randomly selected anti-GPIIb/IIIa Fab clones for κ , λ and Fd chains showed that an Fd chain was present in 12 of the clones (80%) while the λ chain was present in all the clones.

Fab binding to GPIIb/IIIa on platelets was determined quantitatively by preincubating pool phabs with platelets at various concentrations. The supernatant was then analysed by an immunodot method. In this connection, it was established that from 1 to 3×10^4 phabs bind per platelet. This indicates that approximately 10 to 50% of the GPIIb/IIIa molecules per platelet can be occupied by phabs.

1.8. Characterizing the phab-binding epitopes

The epitope specificity of the phabs was determined by carrying out an inhibition test using a variety of monoclonal antibodies (see item 4 [sic]). 1 μ l of thawed normal and thrombasthenic platelets (10^9 /ml), purified GPIIb/IIIa (500 μ g/ml), a peptide fragment of GPIIIa (amino acids 468-690, 500 μ g/ml) and the cytoplasmic segment of GPIIb/IIIa (500 μ g/ml) were in each case added as drops, in duplicate, onto nitrocellulose strips. After blocking, the phab clones (0.4 μ g/ml Fab) were incubated overnight with or

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without monoclonal antibody (1 μ g/ml). The bound phabs were detected using peroxidase-labelled anti-phage antibody and 4-chloro-1- α -naphthol.

- 5 Two groups of phab clones were identified in these investigations. While Group A (5 clones) was inhibited moderately by a pool of all the antibodies, it was inhibited strongly by GPIIb/IIIa complex-specific antibodies. Anti-GPIIb antibodies had no effect. While
- 10 Group B (10 clones) was inhibited completely by the pool of all the antibodies, it was inhibited to a lesser extent by the complex-specific antibody and also by the IIb-specific antibody. No group exhibited any reaction with GPIIIa-specific antibodies. The same
- 15 results were obtained using either platelets or purified GPIIb/IIIa as the antigen. No phab binding to the cytoplasmic peptide or to the extracellular fragment of GPIIIa was found to occur.

A summary of these results is shown in Table 1.

Table 1

Pools of monoclonal antibodies for inhibition	Inhibition of phab binding (mean value \pm SD in %)				
	Group A phab clones (n = 5)		Group B phab clones (n = 10)		
	Platelets	Purified GPIIb/IIIa	Platelets	Purified GPIIb/IIIa	
(1) Anti-GPIIb	0	0	49.1 \pm 5.9	49.4 \pm 9.2	
(2) Anti-GPIIIa	0	0	0	0	
(3) Anti-GPIIb/IIIa complex	77.8 \pm 2.9	43.6 \pm 2.1	58.6 \pm 4.4	45.5 \pm 8.0	
Pool of all the antibodies (1)-(3)	47.6 \pm 7.7	33.0 \pm 10.8	95.9 \pm 2.7	97.5 \pm 7.5	

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1.9. Inhibition assays

The blocking, by the anti-GPIIb/IIIa phabs which had been found, of the binding of patient autoantibodies to GPIIb/IIIa was determined by means of inhibition assays. Two of the phab clones which had been identified as previously described (PDG16 and PDG31) were used for this purpose.

Serial dilutions of the eluted patient autoantibodies of from 1:3 to 1:1000 were analysed for binding to purified GPIIb/IIIa. This was done by performing an immunodot assay. 100 ng of purified GPIIb/IIIa were in each case added as drops, in triplicate, onto nitrocellulose strips and the filters were then blocked with TBS-casein. In order to block the binding of AITP autoantibodies to GPIIb/IIIa with phabs, the strips were incubated with 10^{11} phabs for 1 h and then incubated with varying dilutions of AITP autoantibodies for 4 h. Bound autoantibodies were detected using peroxidase-labelled anti-human IgG-Fc antibodies and ECL.

Anti-GPIIb/IIIa phabs inhibited the binding of autoantibodies obtained from 8 AITP patients. The inhibition range [sic] was [sic] from 10 to 46%, from 32 to 60% and from 20 to 67% for PTG16, PTG31 and the pool of the two phabs, respectively. These phabs had no effect on the binding of autoantibodies obtained from 4 AITP patients. Both groups contained autoantibodies derived from patients suffering from primary AITP and from disease-associated AITP.

The results which were obtained are summarized in Table 2.

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Table 2

	Inhibition of the binding to purified GPIIb/IIIa by (%)		
AITP patient	Phab clone PDG16	Phab clone PDG31	Pool of the two phab clones
WS16	13	19	40
WS37	14	20	36
KC	24	22	28
KK	22	22	40
KP	10	36	60
WS2	25	55	65
KS	60	56	64
KL	0	15	10
KG	0	0	0
KM	0	0	0
KE	0	0	0
KR	0	0	0

1.10 DNA sequence analysis

5

Plasmid DNA was purified from four Group A phab clones and 4 group [lacuna] clones using the Nukleobond® AX PC 20 purification kit (Macherey-Nagel AG, Oensingen, Switzerland).

10

The nucleic acid sequencing was carried out on an ABI373A sequencing system using a PRISM Ready Reaction DyeDeoxy Terminator Cycle Sequencing kit. The primers were obtained from Microsynth, Balgach, Switzerland.

15

The following primers were used for sequencing the H chain: Chy1 (5'-CGC TGT GCC CCC AGA GGT-3') and PCH (5'-GGC CGC AAA TTC TAT TTC AAG G-3'). The following primers were used for sequencing the L chain: Cλ (5'-GAG ACA CAC CAG TGT GGC-3'), Cκ (5'-CAC AAC AGA GGC AGT TCC-3') and PCL (5'-CTA AAC TAG CTA GTC TCC-3'). The amino acid sequences which were deduced from the DNA

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sequence were compared with GenEMBL-Genbank and strain lines were assigned to VH and V λ families.

The VH and V λ nucleotide sequences of the 4 phab clones from each group (Group A: PDG7, PDG8, PDG10 and PDG16; Group B: PDG13, PDG17, PDG31 and PTG37 [sic]) were analysed by automated sequencing and compared with known strain line gene sequences (Tables 3 and 4). There was 100% homology in the deduced amino acid sequences of the H and L chains within each group. By contrast, the homology between Group A and Group B was only 36.9% in the case of the H chain and 81.9% in the case of the L chain amino acid sequences.

In the H chain, Group A clones exhibit the highest degree of sequence identity with the strain line gene VH4.11 of the V_H4 family (Sanz, et al. EMBO J. 8 (1989), 3741-3748). There were 7 amino acid differences in the framework region (FR) and 8 in the complement-determining [sic] region (CDR). Group B clones differed from the mostly homologous 1.9III strain line sequence of the V_H3 family (Berman et al., EMBO J. 7 (1988), 727-738) in four amino acids in the FR and one in the CDR.

25

In the L chain, the Group A and Group B clones exhibited the highest homology with the DPL2 strain line gene sequence of the V λ 1 family (Williams and Winter, Eur. J. Immunol. 323 (1993), 1456). There were nine amino acid differences in FR and ten in CDR in the case of the Group A clones, and one in FR and two in CDR in the case of the Group B clones. The results which were obtained are summarized in Tables 3 and 4.

30

A: Heavy chains

Clones EN1

B. Light chains

Clones FR1

FR: framework region; CDR: complement-determining [sic] region. The top sequences (VH4.11; 1.9III; DPL2) are given for comparative purposes and in each case represent the deduced amino acid sequence for the most closely related published strainline gene sequence. Dashes denote identity. M85255 refers to the EMPL/GenBank reference number and denotes the deduced amino acid sequence of the human anti-GPIIb autoantibody 2E7 (Kunicki et al., J. Autoimmun. 4 (1991), 433-446). In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence.

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Table 4 shows the assignment of the Group A and Group B clones to known strainline V gene sequences in accordance with the amino acid homology

PDG phab clones	Heavy chain			Light chain		
	V _H family	Strain-line gene	Homology (%)	V _L family	Strain-line gene	Homology (5)
Group A: 7,8,10, 16	V _H 4	V _H 4.11	84.3	V _L I	DPL2	81.4
Group B: 13,17, 31,37	V _H 3	1.9III	95.1	V _L I	DPL2	97.1

5

2. Identifying antiidiotypic antibody sequences

2.1 Phab clones AI-X

10 The phagemids technique was used to identify sequences for antiidiotypic antibodies in accordance with the method described in Example 1. The clone PDG16, which was selected in Example 1, was used as the antigen. There was no negative preselection.

15

Use was made of a pool of combinatorial phab libraries [lacuna] the specificities of a nonimmune library of peripheral B lymphocytes and of a library of peripheral lymphocytes which had been immobilized with red blood cells, and also of a nonimmune library of B lymphocytes obtained from tonsils.

20

The pool of phabs which was obtained after the fourth round of panning was analysed. For this, 40 phab clones were selected at random and their binding specificities were determined. 25 of the selected clones reacted with anti-GPIIb/IIIa phab. These antiidiotypic phab clones belong to two groups: Group I (three clones) only

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reacted with Group A autoantibody phab clones (PDG 7, 8, 10 and 16), whereas the Group II phab clones (22 clones in all) reacted with the Group A and Group B phab clones, with murine monoclonal anti-GPIIb/IIIa antibodies, with purified serum immunoglobulin (IVIgG) or F(ab')₂ fragments thereof, and with anti-IgE Fab. 14 phab clones (Group III) did not react with any of the substances mentioned. One Group IV phab clone only reacted with anti-GPIIb/IIIa antibodies. The results of these specificity assays are summarized in Table 5a.

A DNA sequence analysis carried out on Group I phab clones (AI-X16, 17 and 24) showed complete identity in the heavy-chain-encoding sequences apart from one amino acid in the CDR2 region and complete identity in the light-chain-encoding sequences. A comparison with known strainline gene sequences showed approx. 85% homology with the VH3 H chain sequence and approx. 90% homology with the V-λII L chain family sequence. A DNA sequence analysis of the H chain gene was carried out on one representative of each of the Group II, III and IV phab clones. The results of this sequence analysis, and of the comparison with known strainline gene sequences, are summarized in Tables 6 and 7a.

The result of an inhibition assay is depicted in Fig. 1. The inhibition of the binding of AI-X17 to PDG-A by purified GPIIb/IIIa was determined by means of an immunodot assay. 660 and 220 ng of PDG-A phab, respectively, were added to nitrocellulose. The antigen was incubated for 2 h with GPIIb/IIIa at concentrations in the range from 50 μg/ml to 50 ng/ml, and with a buffer solution as control, and then incubated for a further two hours with the phage clone AI-X17 (final concentration 10¹²/ml). The bound phages were detected using peroxidase-conjugated polyclonal rabbit anti-phage antibody and electrochemiluminescence.

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It was found that the AI-X17 phab (Group I) is able to inhibit the binding of Group A antibody phabs (PDG-X) to the IIb/IIIa glycoprotein. This signifies that AI-X17 recognizes the antigen-binding site on PDG-A.

5

Another clone AI-X2 which binds to PDG-A was sequenced. Like clones AI-X20, 39 and 40, this clone only has a heavy chain and no light chain. The heavy chain is able to bind on its own, possibly as a dimer, to the antigen, i.e. PDG-A, with adequate specificity and affinity.

10

2.2 Phab clones AI-B

The phagemid technique was used to identify sequences of other antiidiotypic antibodies in accordance with the method described in Example 2.1. A clone PDG-B which was selected in Example 1 was used as the antigen.

20

In all, 40 phab clones were selected and their binding specificity determined. 34 of the selected clones reacted with anti-GPIIb/IIIa PHAB. These antiidiotypic phab clones belonged to three groups:

25

Group I (14 clones) only reacted with the Group B antibody phab clones, whereas the Group II phab clones (8 clones in all) reacted with both Group A and Group B phab clones. The Group III phab clones (12 clones in all) additionally reacted with murine monoclonal anti-GPIIb/IIIa antibodies, with purified serum immunoglobulin (IVIgG) or F(ab')₂ fragments thereof, and with anti-IgE Fab. Six phab clones (Group IV) did not react with any of the substances mentioned. The results of these specificity assays are summarized in Table 5b.

30
35

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The result of carrying out a DNA sequence analysis on Group I phab clones (AI-14, 18, 24 and 38) is summarized in Tables 6 and 7b. Clones AI-B14, 18 and 38 only had a heavy chain.

5

AI-B14 and 17 are identical. AI-B34 and 40 are likewise identical with AI-B18.

10 The inhibition of the binding of PDG-B to platelets by AI-B phabs is depicted in Fig. 2. This was determined by means of flow-cytometric analysis. For this, a platelet-rich plasma (10^7 platelets in all) was incubated with biotinylated PDG-B in the presence or absence of AI-B phabs and using helper phages as the control. The platelets were fixed with paraformaldehyde and bound PDG-B was detected with R-phycoerythrin (RPE)-labelled streptavidin. 10,000 events were counted in a FACScan appliance and the mean value of the fluorescence (\pm SD) was recorded. The strongest inhibition (> 60%) was achieved with clones AI-B18, 24 and 38. The inhibition of the binding shows that AI-B clones interact with the antigen-binding site on PDG-B.

15

20

Table 5a

Binding to

AIX phab clones		PDG A	PDGB	anti-IgE Fab	anti-GPIIb/IIIa mAb	SG	F(ab') ₂
Group I							
16,17,24	3	+	-	-	-	-	-
Group II							
1,2,3,4,5,6,7,9,11, 13,14,23,26,27,28,29, 33,35,36,37,38,40	22	+	+	+	+	+	+
Group III							
8,10,12,15,18,19,21, 22,25,30,31,32,34,39	14	-	-	-	-	-	-
Group IV							
20	1	-	-	-	+	-	-

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Table 5b

AI-B

phab clones

Binding to

n	PDG-X	PDG-B	anti-IgE Fab	anti-GPIIb/IIIa mAb	IvIgG	IvIgG F(ab') ₂
14						
(AI-B5, 7, 8, 14, 17, 18, 23, 24, 30, 31, 33, 34, 38, 40)	-	+	-	-	-	-
8	+	+	-	-	-	-
12	+	+	+	+	+	+
6	-	-	-	-	-	-

Table 6

anti-Id

phage clones

antiidiotypic

phab clones

(AI-X and AI-B)

	H chain			L chain		
	V _H family	Strainline	Homology	V _L family	Strainline	Homology
		gene	(%)*		gene	(%)*
AI-X16, AI-X24	V _H 3	DP47	88	V _L 2	DPL10	88
AI-X17	V _H 3	DP47	87	V _L 2	DPL10	88
AI-X39	V _H 3	DP49	94	-	-	-
AI-X40	V _H 3	DP31	95	-	-	-
AI-X20	V _H 4	DP71	78	-	-	-
AI-B14, AI-B17	V _H 3	DP46	91	-	-	-
AI-B18	V _H 1	DP10	85	-	-	-
AI-B24	V _H 3	DP49	81	V _L 3	3h	82
AI-B38	V _H 1	DP5	98	-	-	-

* Highest homology (in %) of the amino acid sequences of the respective phab clones with sequences of known strainline V genes

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Table 7a

A. Heavy chains

Clones	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
DP47	EYQLLESGGGLVQPGGSLRLSCAASGFTFS	SYMH	HVRQAPGKLEHVS	AISQSGSTYYADSVKQ	RTTISRDNISKITLYLQHSLRAEDTAVYYCAK		
AIX16	Q-K-----H-----D	HF--	-----	G--Q-LL-H-----	-----H--R--V-----	VADLGIVLSTETEDI	HQGGTKYTVSS
AIX24	-----	-----	-----	-----	-----	-----	-----
AIX17	-----	-----	-----	-----N-----	-----	-----	-----
DP49	QVQLVLSGGGVVQPGRSRLSCAASGFTFS	SYGH	HVRQAPGKLEHVA	VISYDSHKYYADSVKQ	RTTISRDNISKITLYLQHSLRAEDTAVYYCAK		
AIX39	--K-L-----H-----	--T--	-----	L-----	--A-----K-----	DGRSGSYAREDGHV	HQGGTTYTVSS
DP31	EYQLVLSGGGLVQPGRSRLSCAASGFTFD	DYMH	HVRQAPGKLEHVS	GISHISGSGIYADSVKQ	RTTISRDNIAKISLYLQHSLRAEDTAVYYCAK		
AIX10	Q-K-L-----	---L-	-----	---D-T-----	-----V--	HQSSVYATYNAFDI	HQGGTHYTVSS
DP71	QVQLQESGPGLVKPSETLSLTCTVSGGSIS	SYTH	HVRQAPGKLEHIG	YIYYSOSTHYNPSLKS	RVTISVDTSKIQESLKLSSVTAADTAVYYCAR		
AIX20	--K-L-----DV--R	-H--	-L-----	I--DCAR-RT---R-	--SL-H-P-K-----G-----S-----	DADQDGFSPYYFPY	HQGGTPYGVSS

B. Light chains

Clones	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
DPL10	QSALTQPASVSGSPGQSITISC	TGTSSDVGYHIVS	HVQNHGKAPKIHIV	EVSKAPS	GVSHRFSGSKGHITASLTISGLQAEDEADYYC	CSYASSTF	
AIX16	VV-----	---AL-H--F--P	-----	-G-----	-----E--	---VII--H	HVFGGDKLTVLGQPKAAPSVTLFPPSS
AIX24	-----	-----	-----	-----	-----	-----	-----
AIX17	-----	-----	-----	-----	-----	-----	-----

25

FR: framework region; CDR: complement-determining [sic] region. The top sequences (DP47, DP49, DP31, DP71 and DPL10) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence.

Table 7b

A. Heavy chains

Clones	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
DP-46	QVQLVESGGGVVQPGRSRLSCAASGFTFS	SYAHH	HVRQAPGKGLEHVA	VISYDGSNHYADSVKG	RTTISRDNISKNTLYLQNHSLRAEDTAVYYCAK		
AI-B11	--K-L-----	D-G--	-----	A-----	--S-----H-----ST-----T---	DSETAIAAGRTDI	HGQGTHTVVS
AI-B11	-----	-----	-----	-----	-----	-----	-----
DP-10	QVQLVQSGAEVKKPGSSVKVSCASGGTIS	SYAIS	HVRQAPGKGLEHIG	GIIPITGTANYAQKFG	RVITTADESTSTAYHELSSLRSEDVAVYYCAK		
AI-B10	--K-LE-----H-----	-HT-	-----	--T--V-----	-----P-----R--T-DDSGI-----	EDGTVPSQPLEF	HGQGTHTVVS
DP-49	QVQLVESGGGVVQPGRSRLSCAASGFTFS	SYGHH	HVRQAPGKGLEHVA	VISYDGSNHYADSVKG	RTTISRDNISKNTLYLQNHSLRAEDTAVYYCAK		
AI-B21	--K-L---L---Q---S---H---	K-AI-	-----Y-S	A--SH-G-T-----	-----V---S-----VR	GSGLYLGYYIDY	HGQGTHTVVS
DP-5	QVQLVQSGAEVKKPGASVKVSKVSGYTLI	ELSHH	HVRQAPGKGLEHIG	GIIPEDGETIYAQKFG	RVTHTEDTSTDAHELSSLRSEDVAVYYCAT		
AI-B30	Q-K-LE-----	-----	-----	-----	-----	GLRSYHYGRHLDI	HGQGTHTVVS

B. Light chains

Clones	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
VL3h	SYVLTPPSVSVAPGKTARITC	GGHHGSKSVH	WIOOKPGQAPVLVI	YDSRPS	FIPEFSGSHSGNTATITISRVAGDEADYYC	QVHPSSSDH	
AI-B21	-V-----RQ--T---	--YK-----	-----V-	[--Y---	C-----H-----TG-----	---HTH-Q	TITGGTKLTVLAQPKAAPSVTLFPPSS

FR: framework region; CDR: complement-determining [sic] region. The top sequences (DP46, DP10, DP49, DP5 and VL3h) are given for comparative purposes and represent the most closely related known strainline sequences. Dashes denote identity. In the case of the heavy chain, the first three amino acids (QVK) are specified by the pComb3 vector sequence.

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3. Effect of autoantibody polypeptides on the binding of fibrinogen to blood platelets

3.1 Methods

5

Analysis of the binding of Fab to EDTA-pretreated blood platelets

10 A blood platelet-rich plasma was incubated with 10 mM EDTA for 30 min. Biotinylated PDG-B and PDG-A polypeptides were added and the mixture was incubated at room temperature for 1 h. The binding of PDG-A and PDG-B to blood platelets was measured by flow-cytometric analysis using phycoerythrin-labelled
15 streptavidin.

Aggregation experiments

20 Blood platelet-rich plasma ($250 \times 10^9/l$) was prepared freshly and maintained under 5% CO₂. The plasma was activated by different dilutions of ADP (maximum concentration 410 μ M) in the absence or presence of PDG-A or PDG-B (maximum quantity 10 μ g of Fab). The aggregation was measured in a Rodell 300BD-5
25 aggregometer (Baxter AG, Düringen, Switzerland). In subsequent experiments, polyclonal anti-Fab antiserum was added to the activated platelets after PDG-A or PDG-B had been added.

30 Fibrinogen binding test

Wells of ELISA plates were coated with 0.5 μ g/ml GPIIb/IIIa and blocked with 3.5% bovine serum albumin in Tris-buffered salt solution. Fibrinogen (Kabi
35 Diagnostics, Stockholm, Sweden) was then added at different concentrations (maximally 0.08 μ g/ml) in the absence or in the presence of PDG-A, PDG-B or anti-IgE Fab as the control (maximum concentration 23 μ g/ml).

The bound fibrinogen was measured with rat anti-human fibrinogen antibody, biotinylated mouse anti-rat antibody and a conjugate consisting of streptavidin and biotinylated horseradish peroxidase (Amersham Pharmacia Biotech Europe GmbH, Dübendorf, Switzerland) and using an ELISA Easy Reader (EAR340AT, SLT Instruments, Austria) at 405 nm.

Competition assay using the monoclonal antibody 7E3 and the antibody fragment ReoPro®

Platelet-rich plasma ($230 \times 10^9/l$) was incubated for 1.5 h with PDG-B or PDG-A (200 and 400 $\mu g/ml$, respectively) with or without the murine monoclonal antibody 7E3 or its Fab fragment ReoPro® (total quantity of Fab in the range from 10^{14} to 10^{10}). After fixing with an equal volume of 1% paraformaldehyde, the binding of PDG-B and PDG-A to platelets was measured by flow-cytometric analysis using phycoerythrin-labelled streptavidin.

3.2 Results

The recombinant anti-GPIIb/IIIa Fab autoantibody fragments which were tested do not exhibit any binding to blood platelets which had been pretreated with 10 mM EDTA. This shows that the autoantibody fragments only recognize an antigen whose confirmation is intact (Fig. 3).

In aggregation experiments using platelet-enriched plasma, neither PDG-A nor PDG-B inhibited the aggregation. In a fibrinogen-binding test in which the concentration of fibrinogen was from 10^4 to 10^6 times lower than in serum, PDG-A and PDG-B completely inhibited the fibrinogen binding (Fig. 4). No inhibition occurred when anti-IgE Fab, which had been obtained by a similar enrichment protocol, was used as

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the control. These results show that both PDG-A and PDG-B interact powerfully with the fibrinogen-binding site on GPIIb/IIIa.

- 5 In investigations carried out with the murine monoclonal anti-GPIIb/IIIa antibody 7E3 and its commercially available Fab fragment ReoPro[®], both of which inhibit the binding of fibrinogen to activated GPIIb/IIIa, the binding of PDG-B to blood platelets was
- 10 found to be inhibited selectively and completely (Figures 5 to 7). By contrast, the binding of PDG-A to blood platelets was not inhibited significantly either by 7E3 or by ReoPro[®].

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

5 (A) NAME:
ASAT AG Applied Science & Technology
(B) STREET: Baarerstrasse 77
(C) CITY: Zug
(E) COUNTRY: Switzerland
10 (F) POSTAL CODE: 6302

(ii) TITLE OF INVENTION: Recombinant antibodies

(iii) NUMBER OF SEQUENCES: 30

15

(iv) COMPUTER-READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0,
Version #1.30 (EPO)

(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19723904.8
25 (B) APPLICATION DATE: 06-JUN-1997

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(A) APPLICATION NUMBER: DE 19755227.7
(B) APPLICATION DATE: 12-DEC-1997
30

(vi) ORIGINAL APPLICATION DATA:

(A) APPLICATION NUMBER: DE 19820663.1
(B) APPLICATION DATE: 08-MAY-1998

35 (2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 357 base pairs

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- (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) NOTATION: 1..357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CAG	GTG	AAA	CTG	CTC	GAG	TCG	GGC	CCA	GGA	CTG	GTG	AAG	CCT	TCG	GAG	48
Gln	Val	Lys	Leu	Leu	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	
1				5				10					15			
ACC	CTG	TCC	CTC	AAC	TGC	ACT	GTC	TCT	GGT	CGC	TCC	ATC	AGT	GGT	TAC	96
Thr	Leu	Ser	Leu	Asn	Cys	Thr	Val	Ser	Gly	Arg	Ser	Ile	Ser	Gly	Tyr	
			20				25					30				
TCT	TGG	AGA	TGG	ATC	CGG	CAG	TCT	CCA	GGG	AAG	GGA	CTA	GAG	TGG	ATT	144
Ser	Trp	Arg	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
		35				40						45				
GGG	GAT	ATC	TCT	TAT	AGT	GGG	AGT	ACC	AAG	TAC	AAA	CCC	TCC	CTC	AGG	192
Gly	Asp	Ile	Ser	Tyr	Ser	Gly	Ser	Thr	Lys	Tyr	Lys	Pro	Ser	Leu	Arg	
	50				55					60						
AGT	CGA	GTC	ACC	CTG	TCA	GTA	GAC	ACG	TCC	AAG	AAC	CAG	TTC	TCC	CTG	240
Ser	Arg	Val	Thr	Leu	Ser	Val	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	
65				70				75				80				
AAG	CTG	AAT	TCG	GTG	ACC	GCT	GCG	GAC	ACG	GCC	GTC	TAT	TAC	TGT	GCG	288
Lys	Leu	Asn	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
			85				90					95				
CGA	GTC	TTG	CCC	TTT	GAC	CCG	ATC	TCG	ATG	GAC	GTC	TGG	GGC	AAA	GGG	336
Arg	Val	Leu	Pro	Phe	Asp	Pro	Ile	Ser	Met	Asp	Val	Trp	Gly	Lys	Gly	
			100				105					110				
ACC	ACG	GTC	ACC	GTC	TCC	TCA										357
Thr	Thr	Val	Thr	Val	Ser	Ser										
			115													

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Asn Cys Thr Val Ser Gly Arg Ser Ile Ser Gly Tyr
 20 25 30
 Ser Trp Arg Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Asp Ile Ser Tyr Ser Gly Ser Thr Lys Tyr Lys Pro Ser Leu Arg
 50 55 60
 Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Val Leu Pro Phe Asp Pro Ile Ser Met Asp Val Trp Gly Lys Gly
 100 105 110
 Thr Thr Val Thr Val Ser Ser
 115

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 5
- (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15 GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG TGG GTC 48
 Val Val Thr Gln Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
 120 125 130 135
 ACC ATC TCT TGT TCT GGG AGC AGC TCC AAC ATC AGA AGT AAT CCT GTT 96
 Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
 140 145 150
 AGC TGG TAT CAC CAG GTC CCA GGC ACG GCC CCC AAA CTC CTC ATC TTT 144
 Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Ile Phe
 155 160 165
 GGT AGT CAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC 192
 Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 170 175 180
 AAG TCG GGC ACC TCC GCC TCC CTG GCC ATC CGT GGG CTC CAA TCT GGG 240
 Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
 185 190 195

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GAT GCT GGT GAC TAT TAC TGT GCA ACA TGG GAT GAC GGC CTC AAT GGT 298
 Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
 200 205 210 215

CCG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA AGT CAG CCC 333
 Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 220 225 230

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Trp Val
 1 5 10 15

Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Arg Ser Asn Pro Val
 20 25 30

Ser Trp Tyr His Gln Val Pro Gly Thr Ala Pro Lys Leu Leu Ile Phe
 35 40 45

Gly Ser His Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Arg Gly Leu Gln Ser Gly
 65 70 75 80

Asp Ala Gly Asp Tyr Tyr Cys Ala Thr Trp Asp Asp Gly Leu Asn Gly
 85 90 95

Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln Pro
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 115 120 125	48
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 130 135 140	96
GCT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 145 150 155	144
GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 160 165 170 175	192
AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 180 185 190	240
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 195 200 205	288
GCG AGA GCG CTG GGG AGC TGG GGG GGT TGG GAC CAC TAC ATG GAC GTC Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val 210 215 220	336
TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 225 230	369

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg 1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr 20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val 35 40 45
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val 50 55 60
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr 65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Ala Arg Ala Leu Gly Ser Trp Gly Gly Trp Asp His Tyr Met Asp Val 100 105 110
Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser 115 120

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- 10 (A) NAME/KEY: CDS
 (B) LOCATION: 1..333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GTG GTG ACT CAG CCA CCC TCA GCG TCT GGG ACC CCC GGG CAG AGG GTC	48
Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val	
125 130 135	
ACC ATC TCT TGT TCT GGA AGC AGC TCC AAC ATC GGA AGT AAT ACT GTA	96
Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val	
140 145 150 155	
AAC TGG TAC CAG CAG CTC CCA GGA ACG GCC CCC AAA CTC CTC ATC TAT	144
Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr	
160 165 170	
AGT AAT AAT CAG CGG CCC TCA GGG GTC CCT GAC CGA TTC TCT GGC TCC	192
Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser	
175 180 185	
AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC AGT GGG CTC CAG TCT GAG	240
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu	
190 195 200	
GAT GAG GCT GAT TAT TAC TGT GCA GCA TGG GAT GAC AGC CTG AAT GGT	288
Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Ser Ser Leu Asn Gly	
205 210 215	
TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC	333
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro	
220 225 230	

15 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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Val Val Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val
 1           5           10           15
Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr Val
          20           25           30
Asn Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr
      35           40           45
Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
      50           55           60
Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu
 65           70           75           80
Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly
          85           90           95
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
      100           105           110

```

(2) INFORMATION FOR SEQ ID NO: 9:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleotide
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 1..369

15

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

```

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTT CAC CCC GGG GGG      48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
          115           120           125

TCC CTG AGA CTC TCT TGT GCA GCC TCT GGA TTT ACG TTT GAC AAC TTT      96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
          130           135           140

GCC ATG AGC TGG GTC CGC CAG GCT CCA GGG AAG GGG CTG GAG TGG GTC      144
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          145           150           155

TCA GGC ATT AGT GGT GGT GGT CTT TTG ACA CAC TAC GCA GAC TCC GTG      192
Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
          160           165           170           175

AAG GGC CGG TTC ACC ATC TCC AGA AAC AAT TCC AGG AAC ACT GTA TAC      240
Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
          180           185           190

CTA CAA ATG AAC AGC CTG AGA GCC GAA GAC ACG GCC GTG TAT TAT TGT      288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
          195           200           205

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GTG AGA GAT CTG GGC TAT AGA GTA CTT TCG ACT TTT ACT TTT GAT ATC 336
 Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 210 215 220

TGG GGC CAG GGG ACA AAG GTC ACC GTC TCT TCA 369
 Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 225 230

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val His Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asn Phe
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Gly Ile Ser Gly Gly Gly Leu Leu Thr His Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asn Asn Ser Arg Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Arg Asp Leu Gly Tyr Arg Val Leu Ser Thr Phe Thr Phe Asp Ile
 100 105 110

Trp Gly Gln Gly Thr Lys Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..375

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GTG GTG ACT CAG CCT GCC TCC GTG TCT GGG TCT CCT GGA CAG TCG ATC	48
Val Val Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile	
125 130 135	
ACC ATC TCC TGC ACT GGA ACC AGC AGT GCT ATT GGG AAT TAT AAC TTT	96
Thr Ile Ser Cys Thr Gly Thr Ser Ser Ala Ile Gly Asn Tyr Asn Phe	
140 145 150 155	
GTC CCC TGG TAC CAA CAG CAC CCA GGC AAA GCC CCC AAA CTC ATG ATT	144
Val Pro Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile	
160 165 170	
TAT GAG GGC AGT AAG CGG CCC TCA GGG GTT TCT AAT CGC TTC TCT GGC	192
Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly	
175 180 185	
TCC AAG TCT GGC AAC ACG GCC TCC CTG ACA ATC TCT GGG CTC CAG GCT	240
Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala	
190 195 200	
GAG GAC GAG GCT GAG TAT TAC TGC TGC TCA TAT GTT CAT AGT AGC ACT	288
Glu Asp Glu Ala Glu Tyr Tyr Cys Cys Ser Tyr Val His Ser Ser Thr	
205 210 215	
AAT TGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT CAG CCC	336
Asn Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro	
220 225 230 235	
AAG GCT GCC CCC TCG GTC ACT CTG TTC CCA CCC TCC TCT	375
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser	
240 245	

5 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Val Val Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile	
1 5 10 15	
Thr Ile Ser Cys Thr Gly Thr Ser Ser Ala Ile Gly Asn Tyr Asn Phe	
20 25 30	
Val Pro Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu Met Ile	
35 40 45	
Tyr Glu Gly Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe Ser Gly	
50 55 60	
Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu Gln Ala	
65 70 75 80	
Glu Asp Glu Ala Glu Tyr Tyr Cys Cys Ser Tyr Val His Ser Ser Thr	
85 90 95	

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Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

15 CAG GTG AAA CTG CTC GAG TCA GGA CCA GGA CTG GTG AAG CCC TCG GAG 48
 Gln Val Lys Leu Thr Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 130 135 140

ACC CTG TCT CTC ACC TGC ACT GTC TCT GAT GTC TCC ATC AGA AGT CAT 96
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His
 145 150 155

TAC TGG AGT TGG CTC CGG CAG CCC CCA GGG AAG GGA CTG GAG TGG ATT 144
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 160 165 170

GGG TTT ATC TAT GAC GGT GCG AGA ACC AGG TTC AAC CCC TCC CTC AGG 192
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg
 175 180 185

AGT CGA GTC TCC CTT TCA ATG GAC CCA TCC AAG AAG CAG TTT TCC CTG 240
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu
 190 195 200 205

AAA CTG GGG TCT GTG ACC GCT GCG GAC TCG GCC GTC TAC TAC TGT GCG 288
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
 210 215 220

AGA GAC GCG GAT GGA GAT GGC TTC AGC CCA TAC TAC TTT CCC TAC TGG 336
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp
 225 230 235

GGC CAG GGA ATC CCG GTC TCC GTC TCC TCG 366
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser
 240 245

(2) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 122 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Asp Val Ser Ile Arg Ser His
 20 25 30
 Tyr Trp Ser Trp Leu Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Phe Ile Tyr Asp Gly Ala Arg Thr Arg Phe Asn Pro Ser Leu Arg
 50 55 60
 Ser Arg Val Ser Leu Ser Met Asp Pro Ser Lys Lys Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Gly Ser Val Thr Ala Ala Asp Ser Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Ala Asp Gly Asp Gly Phe Ser Pro Tyr Tyr Phe Pro Tyr Trp
 100 105 110
 Gly Gln Gly Ile Pro Val Ser Val Ser Ser
 115 120

5 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
 (B) TYPE: nucleotide
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 15 (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CAG GTG AAA CTC CTC GAG TCT GGG GGA GGC GTG GTC CAC CCT GGG AGG 48
 Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg
 125 130 135
 TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT 96
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 140 145 150
 ACT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG 144
 Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 155 160 165 170
 GCA CTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTC 192
 Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 175 180 185

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AAG GGC CGA TTC GCC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTA TAT	240
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	
GCG AAA GAT GGC CGG AGT GGG AGC TAC GCC AGG TTC GAC GGT ATG GAC	336
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp	
220 225 230	
GTC TGG GGC CAA GGG ACC ACG GTC ACC GTC TCC TCA	372
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
235 240 245	

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val His Pro Gly Arg	15
1 5 10	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	30
20 25	
Thr Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	45
35 40	
Ala Leu Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	60
50 55	
Lys Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	80
65 70 75	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	95
85 90	
Ala Lys Asp Gly Arg Ser Gly Ser Tyr Ala Arg Phe Asp Gly Met Asp	110
100 105 110	
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120	

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 372 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..372

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTA CAG CCT GGC AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg	
125 130 135 140	
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT GAT GAT TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
145 150 155	
GCC CTG CAC TGG GTC CGT CAA GCT CCA GGG AAG GGC CTG GAG TGG GTC	144
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
160 165 170	
TCA GGT ATT AGT TGG GAT AGT GGT ACC ATA GGC TAT GCG GAC TCT GTG	192
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
175 180 185	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC TCC CTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
190 195 200	
CTG CAA ATG AAC AGT CTG AGA GCT GAG GAC ACG GCC TTG TAT TAC TGT	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys	
205 210 215 220	
GTA AAA GAT ATG GGG TCT TCG GTA GTG GCT ACG TAC AAT GCT TTT GAT	336
Val Lys Asp Met Gly Ser Ser Val Val Ala Thr Tyr Asn Ala Phe Asp	
225 230 235	
ATC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	372
Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
240 245	

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr	
20 25 30	
Ala Leu His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Gly Ile Ser Trp Asp Ser Gly Thr Ile Gly Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr	
65 70 75 80	

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GGG ACA ATG GTC ACC GTC TCT TCA
 Gly Thr Met Val Thr Val Ser Ser
 240

360

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gln Val Lys Leu Leu Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Phe Ser Thr Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Leu Arg Asn Asp Gly Trp Asn Asp Gly Phe Asp Ile Trp Gly Gln
 100 105 110
 Gly Thr Met Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

25 (vii) IMMEDIATE SOURCE:

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(B) CLONE(E): AI-B14

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 14

5 (B) MAP POSITION: q32.3

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..369

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Val Val Gln Pro Gly Arg	
125 130 135	
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT GAC TAT	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr	
140 145 150	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
155 160 165	
GCA GCT ATA TCA TAT GAT GGA AGT AAC AAA TAC TAT GCA GAC TCC GTG	192
Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
170 175 180	
AAG GGC CGA TTC TCC ATC TCC AGA GAC AAT TCC AAC AAT ACG CTA TAT	240
Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr	
185 190 195 200	
CTG CAA ATG AGC ACC CTG AGA GCT GAG GAC ACG GCT GTC TAT TTC TGT	288
Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys	
205 210 215	
GCG AGA GAT TCG GAA ACG GCA ATA GCG GCA GCT GGA CGG TTT GAT ATC	336
Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile	
220 225 230	
TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA	369
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser	
235 240	

(2) INFORMATION FOR SEQ ID NO: 22:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Asn Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Thr Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95
 Ala Arg Asp Ser Glu Thr Ala Ile Ala Ala Ala Gly Arg Phe Asp Ile
 100 105 110
 Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

15 (vii) IMMEDIATE SOURCE:

(B) CLONE(E): AI-B18

(viii) POSITION IN THE GENOME:

- 20 (A) CHROMOSOME/SEGMENT: 14
 (B) MAP POSITION: q32.3

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..366

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG TCC Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 125 130 135	48
TCG GTG ATG GTC TCC TGC AAG GCT TCT GGA GGC ACC TTC AGC AGC CAT Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser His 140 145 150 155	96
ACT ATC AGC TGG GTG CCG CAG GCC CCT GGA CAA GGC CTT GAG TGG ATG Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 160 165 170	144
GGA GGG ATC ACC CCT ATC TTT GGT ACA GTG AAC TAC GCA CAG AAG TTC Gly Gly Ile Thr Pro Ile Phe Gly Thr Val Asn Tyr Ala Gln Lys Phe 175 180 185	192
CAG GGC AGA GTC ACC ATT ACC GCG GAC GAA CCC ACG AGC ACA GCC TAC Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Pro Thr Ser Thr Ala Tyr 190 195 200	240
ATG GAA CTG AGG AGC CTG ACA TCT GAC GAC TCG GGC ATC TAT TAC TGT Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Gly Ile Tyr Tyr Cys 205 210 215	288
GGC AGA GAA GAT GGC ACT ACA GTA CCA AGT CAA CCC CTT GAG TTC TGG Ala Arg Glu Asp Gly Thr Thr Val Pro Ser Gln Pro Leu Glu Phe Trp 220 225 230 235	336
GGC CAG GGA ACC CGG GTC ACC GTC TCC TCT Gly Gln Gly Thr Arg Val Thr Val Ser Ser 240 245	366

(2) INFORMATION FOR SEQ ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15
Ser Val Met Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser His 20 25 30
Thr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45
Gly Gly Ile Thr Pro Ile Phe Gly Thr Val Asn Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Pro Thr Ser Thr Ala Tyr 65 70 75 80
Met Glu Leu Arg Ser Leu Thr Ser Asp Asp Ser Gly Ile Tyr Tyr Cys 85 90 95
Ala Arg Glu Asp Gly Thr Thr Val Pro Ser Gln Pro Leu Glu Phe Trp 100 105 110
Gly Gln Gly Thr Arg Val Thr Val Ser Ser 115 120

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(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

5 (B) TYPE: nucleotide

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA for mRNA

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

15 (B) CLONE(E): AI-B24

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 14

(B) MAP POSITION: q32.3

20

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..363

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CAG GTG AAA CTG CTC GAG TCT GGG GGA GGC TTG GTC CAG CCT GGG GGG	48
Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
125 130 135	
TCC CTG AGA CTC TCC TGT TCA GCC TCT GGA TTC ACC TTC AAT AAA TAT	96
Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr	
140 145 150	
GCA ATA CAC TGG GTC CGC CAG GCT CCA GGG AAG GGA CTG GAA TAT GTT	144
Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val	
155 160 165 170	
TCA GCT ATT AGT AGT AAT GGG GGT AAC ACA TAC TAC GCA GAC TCC GTG	192
Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val	
175 180 185	
AAG GGC AGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG GTG TAT	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr	
190 195 200	
CTT CAA ATG AGC AGT CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT	288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
205 210 215	
GTT AGA GGA AGT GGG AGC TAC TTA GGA TAC TAC TTT GAC TAC TGG GGC	336
Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly	
220 225 230	

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CAG GGA ACC CTG GTC ACC GTC TCC TCA
 Gln Gly Thr Leu Val Thr Val Ser Ser
 235 240

363

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gln Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Asn Lys Tyr
 20 25 30
 Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Tyr Val
 35 40 45
 Ser Ala Ile Ser Ser Asn Gly Gly Asn Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Arg Gly Ser Gly Ser Tyr Leu Gly Tyr Tyr Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleotide
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA for mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

25 (vii) IMMEDIATE SOURCE:

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(B) CLONE(E): AI-B24

(viii) POSITION IN THE GENOME:

(A) CHROMOSOME/SEGMENT: 22

5 (B) MAP POSITION: q11

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..366

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GTG	GTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	GCT	CCA	AGA	CAG	ACG	GCC	48
Val	Val	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Arg	Gln	Thr	Ala	
			125					130					135			
ACG	ATT	ACC	TGT	GGG	GGA	TAC	AAG	ATT	GGA	AGT	AAA	AGT	GTC	CAC	TGG	96
Thr	Ile	Thr	Cys	Gly	Gly	Tyr	Lys	Ile	Gly	Ser	Lys	Ser	Val	His	Trp	
			140				145					150				
TAC	CAA	CAG	AAG	CCA	GCC	CAG	GCC	CCT	GTA	TTG	GTC	GTC	TAT	GAG	GAT	144
Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr	Glu	Asp	
			155			160					165					
TCC	TAC	CGG	CCC	TCA	GAG	ATC	CCT	GAG	CGA	TTC	TCT	GGC	TCC	AAC	TCT	192
Ser	Tyr	Arg	Pro	Ser	Glu	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Asn	Ser	
					175					180					185	
GGG	AAC	ATG	GCC	ACC	CTG	ACC	ATC	ACC	GGG	GTC	GAA	GCC	GGG	GAT	GAG	240
Gly	Asn	Met	Ala	Thr	Leu	Thr	Ile	Thr	Gly	Val	Glu	Ala	Gly	Asp	Glu	
			190					195					200			
GCC	GAC	TAC	TAC	TGT	CAG	GTG	TGG	GAT	AAT	ACT	AAT	GAT	CAG	ACG	ATA	288
Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Asn	Thr	Asn	Asp	Gln	Thr	Ile	
			205				210						215			
TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	CGT	CAG	CCC	AAG	GCT	GCC	336
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg	Gln	Pro	Lys	Ala	Ala	
			220			225						230				
CCC	TCG	GTC	ACT	CTG	TTC	CCG	CCC	TCC	TCT							366
Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser							
			235			240										

15 (2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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Val Val Thr Gln Pro Pro Ser Val Ser Val Ala Pro Arg Gln Thr Ala
 1 5 10 15
 Thr Ile Thr Cys Gly Gly Tyr Lys Ile Gly Ser Lys Ser Val His Trp
 20 25 30
 Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr Glu Asp
 35 40 45
 Ser Tyr Arg Pro Ser Glu Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser
 50 55 60
 Gly Asn Met Ala Thr Leu Thr Ile Thr Gly Val Glu Ala Gly Asp Glu
 65 70 75 80
 Ala Asp Tyr Tyr Cys Gln Val Trp Asp Asn Thr Asn Asp Gln Thr Ile
 85 90 95
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala
 100 105 110
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 115 120

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 366 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: cDNA for mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens
- 15 (vii) IMMEDIATE SOURCE:
- (B) CLONE(E): AI-B38
- (viii) POSITION IN THE GENOME:
- (A) CHROMOSOME/SEGMENT: 14
- 20 (B) MAP POSITION: q32.3
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 1..366
- 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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CAG GTG AAA CTG CTC GAG TCT GGG GCT GAG GTG AAG AAG CCT GGG GCC Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 125 130 135	48
TCA GTG AAG GTC TCC TGC AAG GTT TCC GGA TAC ACC CTC ACT GAA TTA Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu 140 145 150	96
TCC ATG CAC TGG GTG CGA CAG GCT CCT GGA AAA GGG CTT GAG TGG ATG Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met 155 160 165 170	144
GGA GGT TTT GAT CCT GAA GAT GGT GAA ACA ATC TAC GCA CAG AAA TTC Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe 175 180 185	192
CAG GGC AGA GTC ACC ATG ACC GAG GAC ACA TCT ACA GAC ACG GCC TAC Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr 190 195 200	240
ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC ACG GCC GTG TAT TAC TGT Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 205 210 215	288
GAG ACA GGT CTG AGG TCG TAC AAC TAT GGT CGT AAC CTT GAC TAT TGG Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp 220 225 230	336
GGC CAG GGA ACC CTG GTC ACC GTC TCC TCA Gly Gln Gly Thr Leu Val Thr Val Ser Ser 235 240	366

(2) INFORMATION FOR SEQ ID NO: 30:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Gln Val Lys Leu Leu Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15
Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu 20 25 30
Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met 35 40 45
Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Ile Tyr Ala Gln Lys Phe 50 55 60
Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala Tyr 65 70 75 80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95
Glu Thr Gly Leu Arg Ser Tyr Asn Tyr Gly Arg Asn Leu Asp Tyr Trp 100 105 110

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Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120		

Claims

1. Nucleic acid which encodes a heavy chain, which is able to bind to GPIIb/IIIa, of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:
 - (a) a nucleotide sequence which encodes the amino acid sequence:
V L P F D P I S M D V, (I)
 - (b) a nucleotide sequence which encodes the amino acid sequence
A L G S W G G W D H Y M D V, (II)
 - and
 - (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).
2. Nucleic acid according to Claim 1, which furthermore comprises a CDR1 region selected from:
 - (a) a nucleotide sequence which encodes the amino acid sequence:
G Y S W R, (III)
 - (b) a nucleotide sequence which encodes the amino acid sequence:
S Y A M H, (IV)
 - and
 - (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).
3. Nucleic acid according to either Claim 1 or 2, which furthermore comprises a CDR2 region, selected from.

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- (a) a nucleotide sequence which encodes the amino acid sequence:
D I S Y S G S T K Y K P S L R S, (V)
 - (b) a nucleotide sequence which encodes the amino acid sequence:
V I S Y D G S N K Y Y A D S V K G, (VI)
and
 - (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).
4. Nucleic acid which encodes a light chain, which is able to bind to GPIIb/IIIa, of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:
- (a) a nucleotide sequence which encodes the amino acid sequence:
A T W D D G L N G P V, (VII)
 - (b) a nucleotide sequence which encodes the amino acid sequence
A A W D D S L N G W V, (VIII)
and
 - (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b),

with the proviso that when the nucleic acid encompasses a nucleotide sequence according to (b), it does not simultaneously comprise nucleotide sequences which encode the amino acid sequences SGSSSNIGSNTVN and SNNQRPS, and when the nucleic acid comprises a nucleotide sequence according to (c), it does not simultaneously comprise nucleotide sequences which encode the amino acid sequences SGSSSNIGSNTVN and RNNQRPS.

5. Nucleic acid according to Claim 4, which furthermore comprises a CDR1 region selected from:

(a) a nucleotide sequence which encodes the amino acid sequence:

S G S S S N I R S N P V S, (IX)

(b) a nucleotide sequence which encodes the amino acid sequence:

S G S S S N I G S N T V N, (X)

and

(c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).

6. Nucleic acid according to Claim 4 or 5, which furthermore comprises a CDR2 region selected from:

(a) a nucleotide sequence which encodes the amino acid sequence:

G S H Q R P S, (XI)

(b) a nucleotide sequence which encodes the amino acid sequence:

S N N Q R P S, (XII)

and

(c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% with an amino acid sequence from (a) or (b).

7. Nucleic acid which encodes the heavy chain of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR3 region, selected from:
- (a) a nucleotide sequence which encodes the amino acid sequence:
V R D L G Y R V L S T F T F D I, (XIII)
 - (b) a nucleotide sequence which encodes the amino acid sequence:
D G R S G S Y A R F D G M D V, (XIV)
 - (c) a nucleotide sequence which encodes the amino acid sequence:
M G S S V V A T Y N A F D I, (XV)
 - (d) a nucleotide sequence which encodes the amino acid sequence:
D A D G D G F S P Y Y F P Y, (XVI)
 - (e) a nucleotide sequence which encodes the amino acid sequence:
L R N D G W N D G F D I, (XVII)
 - (f) a nucleotide sequence which encodes the amino acid sequence:
D S E T A I A A A G R F D I, (XVIII)
 - (g) a nucleotide sequence which encodes the amino acid sequence:
E D G T T V P S Q P L E F, (XIX)

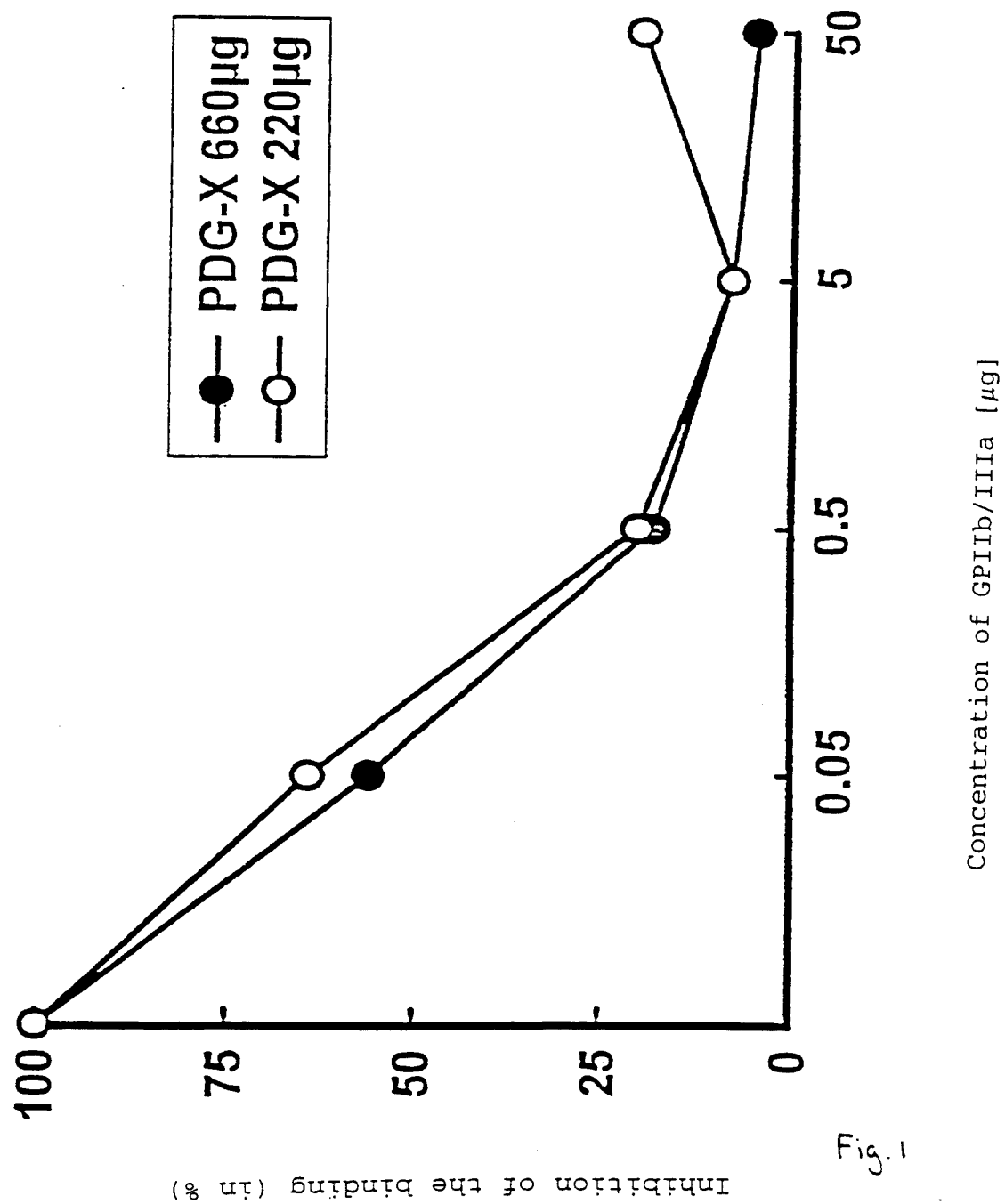
- (h) a nucleotide sequence which encodes the amino acid sequence:
G S G S Y L G Y Y F D Y, (XX)
- (i) a nucleotide sequence which encodes the amino acid sequence:
G L R S Y N Y G R N L D Y, (XXI)
- (j) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80% and preferably of at least 90%, with an amino acid sequence from (a), (b), (c) or (d), and
- (k) a nucleotide sequence which encodes an amino acid sequence having an equivalent ability to bind to autoantibodies against GPIIb/IIIa.
8. Nucleic acid according to Claim 7, which furthermore comprises a CDR1 and/or CDR2 region selected from a nucleotide sequence which encodes the amino acid sequences shown in Tab. 7a or b or an amino acid sequence which is at least 80% homologous thereto.
9. Nucleic acid which encodes the light chain of a human antibody, or a functional derivative or a fragment thereof, and comprises a CDR 3 region, selected from:
- (a) a nucleotide sequence which encodes the amino acid sequence:
C S Y V H S S T N, (XXII)
- (b) a nucleotide sequence which encodes the amino acid sequence:
Q V W D N T N D Q, (XXIII)
- (c) a nucleotide sequence which encodes an amino acid sequence having an homology of at least 80%, and preferably at least 90%, with an amino acid sequence from (a), and
- (d) a nucleotide sequence which encodes an amino acid sequence having an equivalent ability to bind to autoantibodies against GPIIb/IIIa.

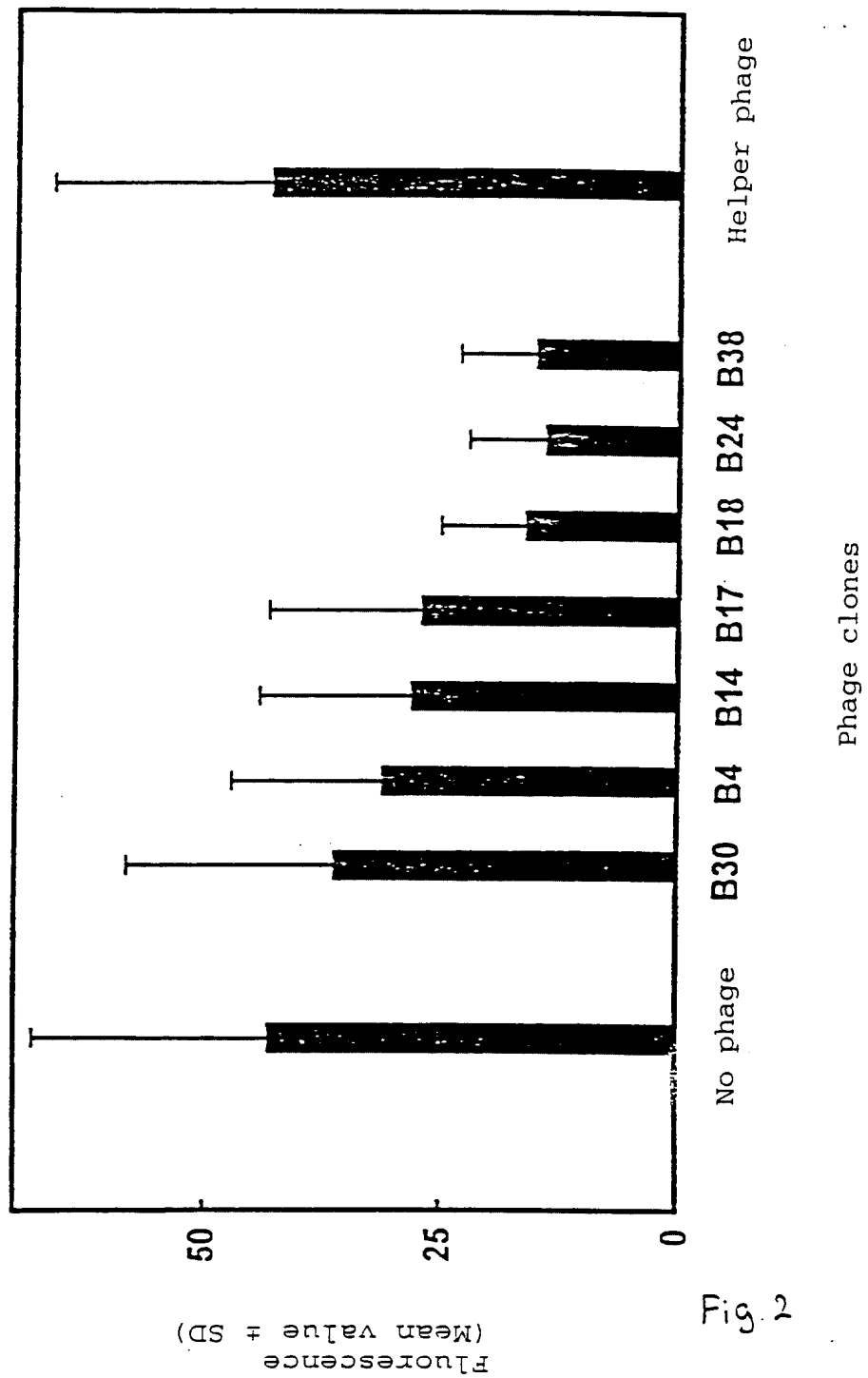
10. Nucleic acid from Claim 9, which furthermore encompasses a CDR1 and/or CDR2 region selected from a nucleotide sequence which encodes the amino acid sequences shown in Tab. 7a or b or an amino acid sequence which is at least 80% homologous thereto.
11. Vector, characterized in that it
 - (a) contains at least one copy of a nucleic acid according to one of Claims 1 to 3 and/or at least one copy of a nucleic acid according to one of Claims 4 to 6 or
 - (b) contains at least one copy of a nucleic acid according to Claim 7 or 8 and/or at least one copy of a nucleic acid according to Claim 9 or 10.
12. Cell, characterized in that it
 - (a) expresses a nucleic acid according to one of Claims 1 to 3 and/or a nucleic acid according to one of Claims 4 to 6 or
 - (b) a nucleic acid according to Claim 7 or 8 and/or a nucleic acid according to Claim 9 or 10.
13. Polypeptide, characterized in that it
 - (a) is encoded by a nucleic acid according to one of Claims 1 to 3 and/or a nucleic acid according to one of Claims 4 to 8 or
 - (b) by a nucleic acid according to Claim 7 or 8 and/or a nucleic acid according to Claim 9 or 10.

14. Polypeptide according to Claim 13, characterized in that it comprises the variable domain of the H chain and/or the variable domain of the L chain of a human antibody.
15. Polypeptide according to Claim 14, characterized in that it comprises both the variable domain of the H chain and the variable domain of the L chain.
16. Polypeptide according to one of Claims 13 to 15, characterized in that it is coupled to a labelling group or a toxin.
17. Antibody against a polypeptide according to one of Claims 13 to 16.
18. Antibody according to Claim 17, characterized in that it is directed against the CDR3 region of the heavy and/or light antibody chain of the polypeptide.
19. Pharmaceutical composition which comprises, as the active component, a nucleic acid according to one of Claims 1 to 10, a vector according to Claim 11, a cell according to Claim 12, a polypeptide according to one of Claims 13 to 16 or an antibody according to either Claim 17 or 18, where appropriate together with other active components and pharmaceutically customary adjuvants, additives or excipients.
20. Use of a nucleic acid according to one of Claims 1 to 10, of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to one of Claims 13 to 16, of an antibody according to Claim 17 or 18, or of a pharmaceutical composition according to Claim 19 for preparing an agent for the diagnosis or for the treatment or prevention of AITP.

21. Use of a nucleic acid according to one of Claims 1 to 10, of a vector according to Claim 11, of a cell according to Claim 12, of a polypeptide according to one of Claims 13 to 16, or of a pharmaceutical composition according to Claim 19 for preparing an agent for exerting an effect on the binding of fibrinogen to blood platelets.
22. Use according to Claim 21 for preparing an agent for modulating blood coagulation, in particular for dissolving thrombi and/or for preventing the formation of thrombi.
23. Process for isolating phagemid clones which express nucleic acids which encode autoantibodies against GPIIb/IIIa or encode antiidiotypic antibodies which are directed against these autoantibodies, characterized in that a phagemid library is prepared from lymphocytes obtained from a healthy human donor and the desired phagemid clones are isolated by affinity selection comprising negative and positive selection steps.
24. Process according to Claim 23, characterized in that antibody-encoding nucleic acids are isolated from the clones.
25. Process according to Claim 23 or 24, characterized in that the antibody-encoding nucleic acids are used for expressing recombinant antibody chains, or derivatives or fragments thereof.

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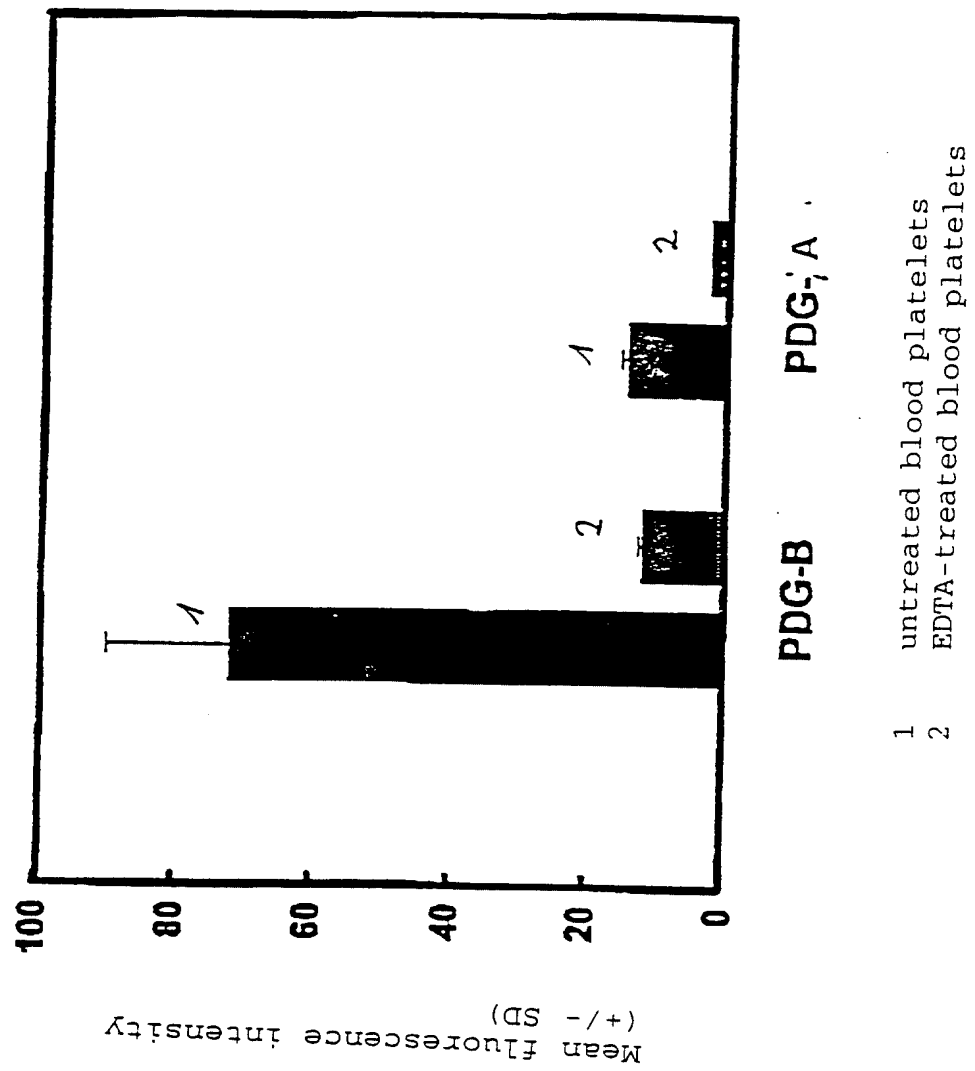
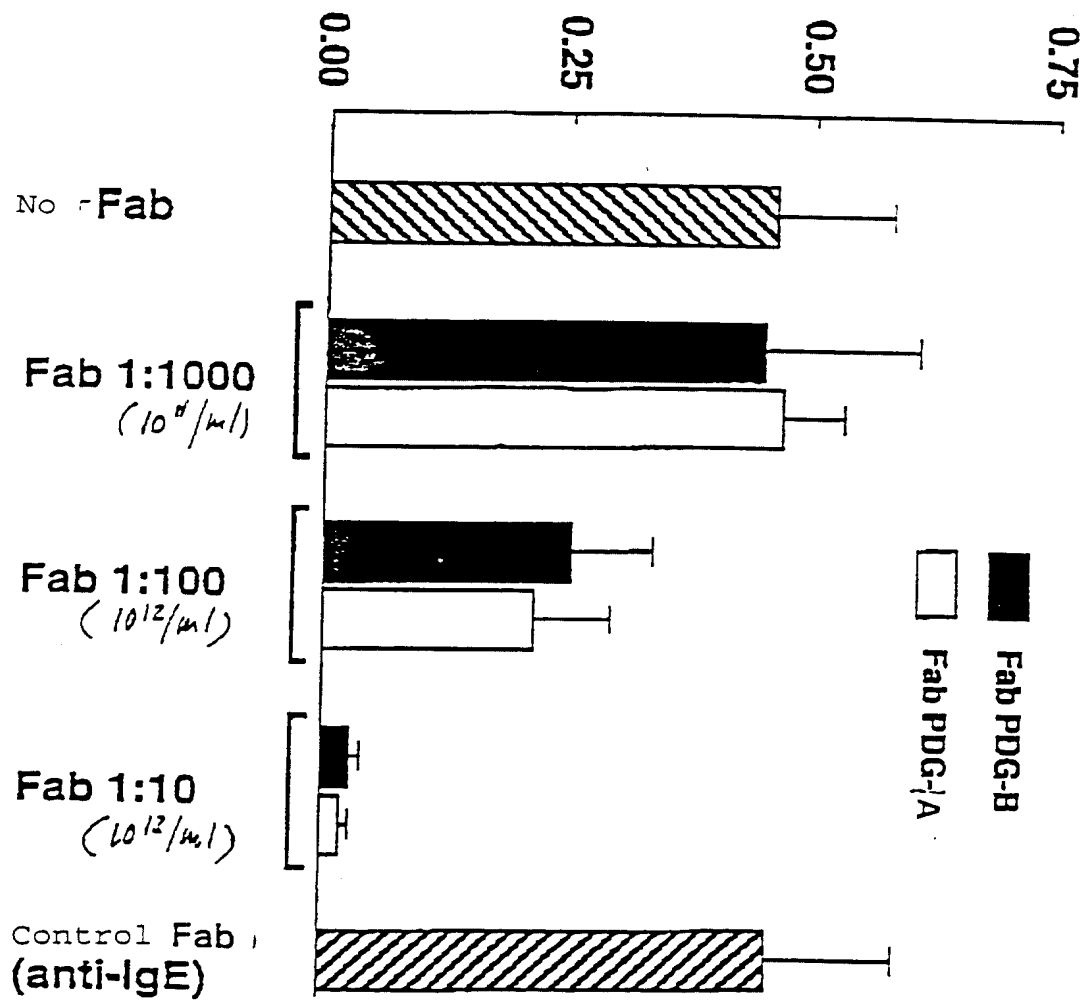


Fig.3

Fibrinogen binding
(mean O/D \pm SD)

Fig. 4



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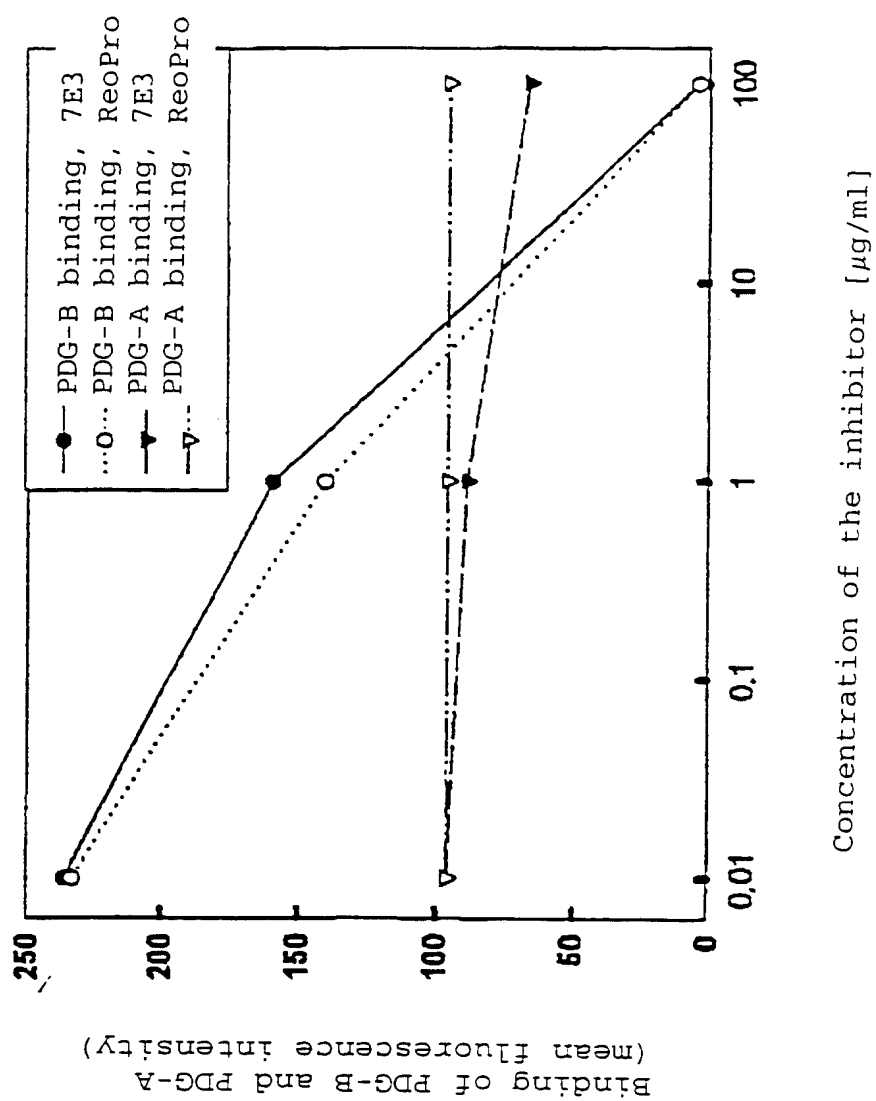


Fig. 5

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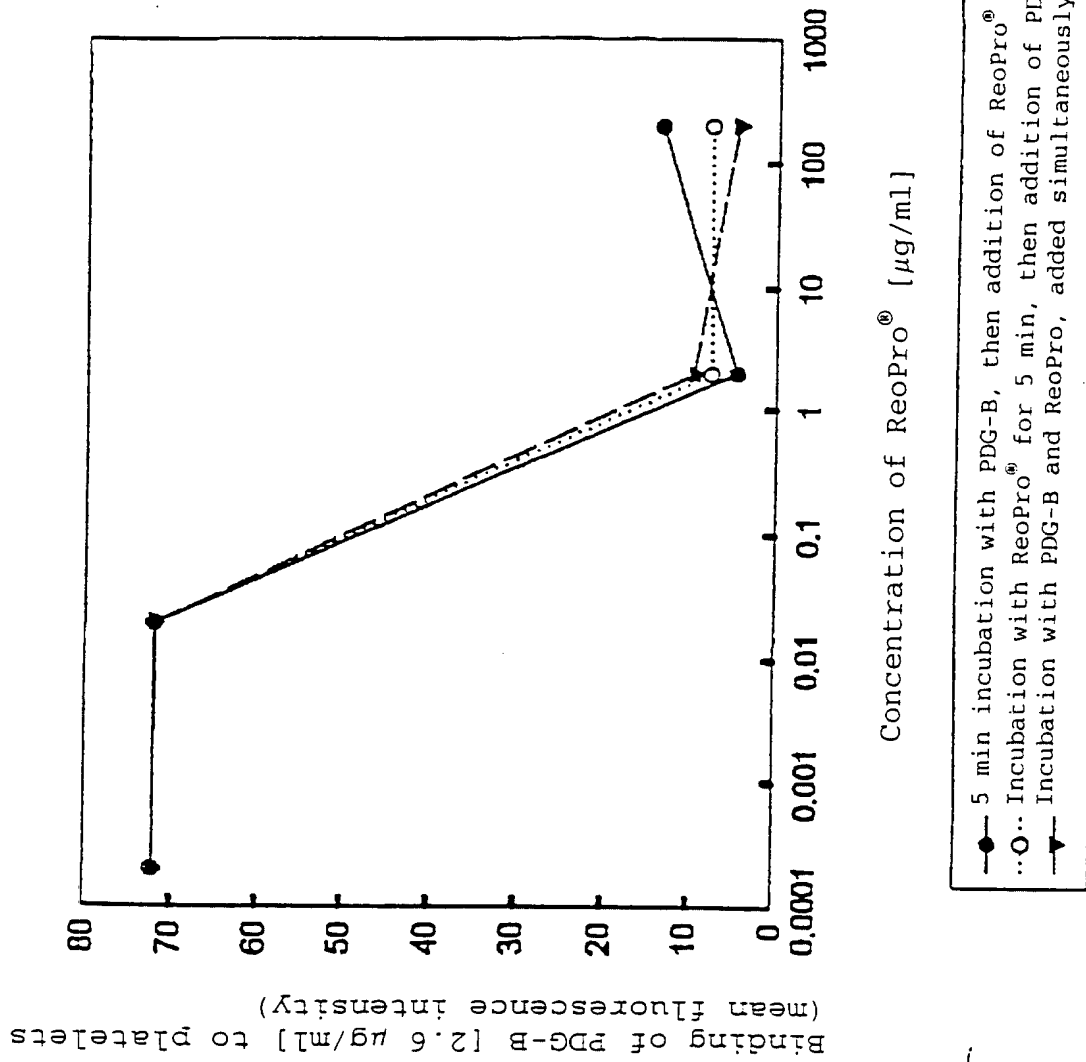


Fig. 6

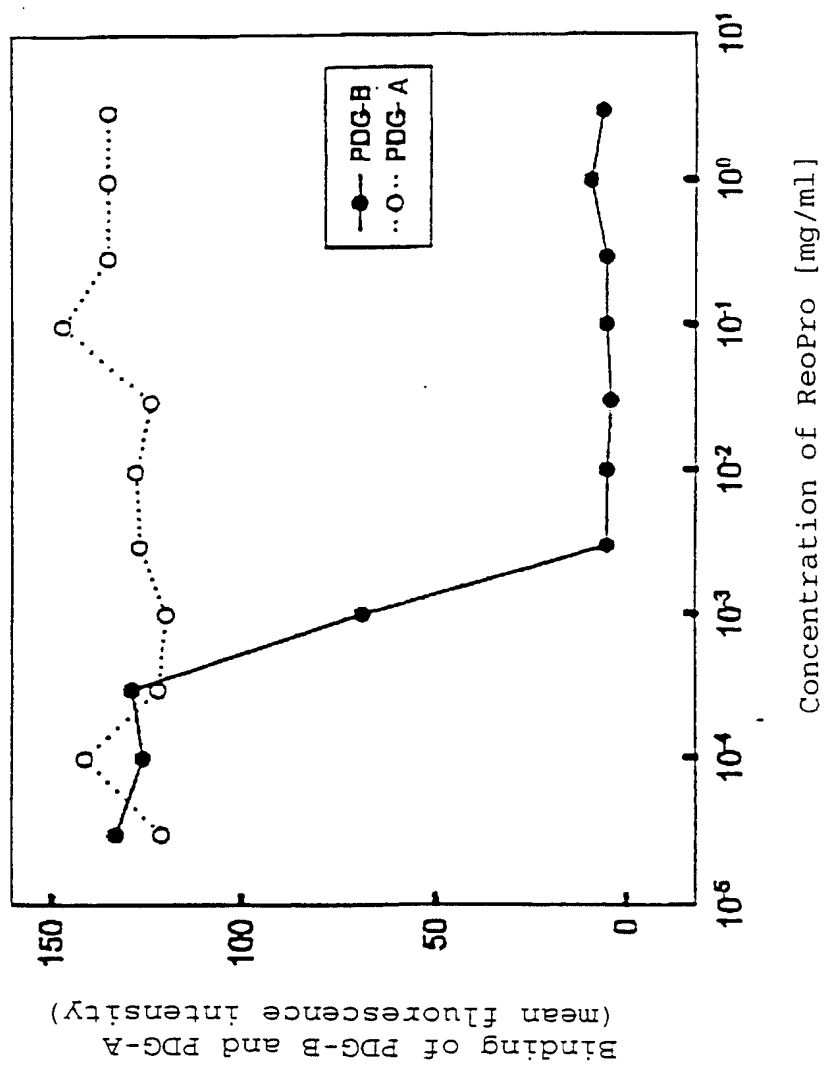


Fig. 7